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Db 79 EISFFHIGSILTSYKDAISYPO-GIKLNOVTKDAGEISCEYTSIGTVLYGEAXIQL 137
Qy 134 TVQYKVPYVPCRVKAVPVGMATLHCQSESGHPRPHYSWYRNDVPLPTDSRANPFRNS 193
Db 138 QVIAVPGTVAQVSSARATSGVALMCEVNGFPLPFTYVHNNSPWAQAS-----QNS 191
Qy 194 SSHANSEIGTVFAVYAKHDSGQYCIASNDAGARCEBQMEYVDLNTIGIIGVLYVL 253
Db 192 TYTIDPNTGVAKFASVGSVDSGEYCKATNSQEGSSAIVAMVDKVNAGIYAAYVIVL 251
Qy 254 AVALLITLIGICCAVRGYFINNKODGESYKPKPGDCVNIYRDEEGDFRHKSFVI 310
Db 252 LIALLLGGLWFAISRGYLDKKNKKVYISQPSF-----TRSDKXFCQTSFVLY 300

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RESULT 14

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Qy5B2 PRELIMINARY; PRT; 259 AA.
AC Qy5B2;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Junction adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Nisbet A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;

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Query Match 20.2%; Score 331; DB 4; Length 259;
Best Local Similarity 29.6%; Pred. No. 4.8e-24;
Matches 81; Conservative 44; Mismatches 111; Indels 38; Gaps 7;

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Qy 42 VVOEFSEVELSCITDSDPTDRIEMKKIODECTVYFNDKIQGLAGRAEILGKTSLK 101
Db 19 ILPENNVKLSCAV--SGFSRPR--AAYEDRATFL-----PTGIT 55
Qy 102 IWAYTRDSALYRCGVAVARNDKEIDEIVELTVQVAVTPVPCRVKAVPVGMATLHCQ 161
Db 56 FKSYTRSDTGTTC-VWFEKGNSYGEVYKYLIVLPSPKPTVINIPSSATIGRAVLTC 114
Qy 162 ESEGHPRPHYSWYRNDVPLPTDSRANPFRNSSHLNSETGLVFTAVHKHDSGQYCI 221
Db 115 EQDGSPPSEYTWFDGIVMTNPKSTAFSNSSVLNPFTGELVFDPLASDTEGYSCE 174
Qy 222 SNDAGARCEBQ-EMEYVDLNTIGIIGVLYVLAVLALITLIGICCAVRGYFINNKQDE 280
Db 175 RNGYGTPTNSAAMEAVERNVGIYAAYVITLILGILVFGIMFAYSRGHFRTKKGTS 234
Qy 281 S-----YKPGKPGCVNIYRDEEGDFRHKSFVI 310
Db 235 SKKYIYISQPS-----ARSGEFGKQTSFVLY 259

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RESULT 15
Qy5B2 PRELIMINARY; PRT; 173 AA.
AC Qy5B2;

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Junctional adhesion molecule (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirsch T., Wellner M., Haller H., Lipoidt A.;
RT "Cloning of the rat junctional adhesion molecule (JAM).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241261; AAF61729.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER
SQ SEQUENCE 173 AA; 18706 MW; 3EB3ECD7A5AFB8B2 CRC64;

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Query Match 19.6%; Score 321; DB 11; Length 173;
Best Local Similarity 40.3%; Pred. No. 2.7e-23;
Matches 71; Conservative 27; Mismatches 72; Indels 6; Gaps 3;

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Qy 137 VKPVPVPCRVKAVPVGMATLHCQSESGHPRPHYSWYRNDVPLPTDSRANPFRNSS 195
Db 2 VPSKPTVTSVTSVITGNRAVLTCSEHDSPPSESWKQGVPLTADAKKTRAFINSSY 61
Qy 196 HLNSETGLVFTAVHKHDSGQYCIASNDAGSA-RCEBQMEYVDLNTIGIIGVLYLA 254
Db 62 TIDPSGLVDPVSAFDSGEYCEAQVGTARSEAVREAVELNAGIYAAYVITLI 121
Qy 255 VLALITLIGICCAVRGYFINNKODGESYKPKPGDCVNIYRDEEGDFRHKSFVI 310
Db 122 LIGLIFGIWFAISRGYLDKKNKKVYISQPSARSGEFGKQTSFVLY 173

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Search completed: April 12, 2004, 09:16:12
Job time : 47 secs

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OY 83 KIGDLAGRARIKTSIKXINWTRBDALYRCEVANDRKEIDEIVIELTVQYKVP 142
DB 77 SLTPPYKRA-IPTPGITLTKQTRKODAGEYCEVTSTGSLTYGEAKIQOYIVAFSK 135
OY 143 VCRVPAVPGKATLHCQESGHPRHYSWYRNDVPLPTDSRANPRFNSSHLSETG 202
DB 136 VAQVPRSVSTGSVALLCVENDGYPPPTFIWYRKSPM---QIAP--QKSTYIDPKTG 189
OY 203 TLVPTAVKXDSGGGYCCIASNDASARCEBEMEVYLNIGTIGLVLATLALITLG 262
DB 190 VLKFAAVSTDSGSEYCEALINNGKQASDLVRMDVQVNVGIVAALVILLIALLIGFG 249
OY 263 ICCAYRRGYFINNKODGESYKNGPKPDGVNRYRTDEGDFRHKSSFEVI 310
DB 250 MFPAYSRGYLDRENKVKYISLPSE-----TRSDKNFGQISSFLV 269

RESULT 12
O8VC39 PRELIMINARY; PRT; 300 AA.
ID O8VC39;
AC 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DB Hypothetical protein (junction cell adhesion molecule1).
GN F1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RA Strausberg R.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RA MEDLINE=22345483; PubMed=12468851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; BC021876; AAH21876.1;
DR EMBL; AK033574; BAC28369.1;
DR MGI; MGI:1321398; F1R.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SMO0406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE_2.
DR Hypothetical protein.
KW SEQUENCE 300 AA; 32423 MW; 3CE56188FFB3B97EC CRC64;

Query Match 27.5%; Score 449.5; DB 11; Length 300;
Best Local Similarity 35.2%; Pred. No. 1,3e-35;
Matches 103; Conservative 56; Mismatches 122; Indels 15; Gaps 7;

OY 20 LLLIFRGLIGAV---NIKSNRTFVVOEFSEVELSCIITDSDPRIEMWKIODE 74
DB 11 LLEFTSMILGSIVOGKGYTAQSDVQVPEHESIKLTC--TVSGFSSPREVEMKFPQGST 68
OY 75 TTVYFPFNKIQGDLAGEAELIGKTSLKINWTRBDALYRCEVANDRKEIDEIVIELT 134
DB 69 TALVCYSQITARYADRV-TFSSSGITFSSVYTRKNGEYTC-WVSEGGQNGEVSIIHT 126
OY 135 VQVQVPTVPCRVPAVPGKATLHCQESGHPRHYSWYRNDVPLPT-DSRANPRFNS 193
DB 127 VLVPSPKRTISVSSSVTIGRAVLTCEHDSPPSEYSWFKDGISMLTADAKTRAFNKS 186
OY 194 SSHLNSGTGLVPTAVAKDSDSGYYCCIASNDASGA-RCEGEQEVYDNLNIGTIGVAVV 252
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DB 187 SFTIDKSGDLIFDPYAFDSEGYCQANGYGTARREBAHMAADVAELNVGIVAALVIT 246
OY 253 LAVALITLIGICAYRRGYFINNKODGESYKNGPKPDGVNRYRTDEGDFRHKSSFEVI 310
DB 247 LILLGLIGVWFAFSRGYFERTKGG-----TAPGKVIYSQSTNSRSGFKGTSSFLV 300

RESULT 13
O7SYQ7 PRELIMINARY; PRT; 300 AA.
ID O7SYQ7;
AC 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DB Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA MEDLINE=22341132; PubMed=12454917;
RA Klein S.L.; Strausberg R.L.; Wagner L.; Pontius J.; Clifton S.W.;
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Peingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Sherman C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Cantinot P.; Prange C.;
RA Baha S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Boek S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton E.; Ketterman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickinson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smallus D.B.; Schnerch A.; Schein J.E.;
RA Jones S.J.; Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S.; Strausberg R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054305; AAH54305.1;
DR Hypothetical protein.
KW NON TER
FT SEQUENCE 300 AA; 32658 MW; 02BC49DC74E271D4 CRC64;

Query Match 26.6%; Score 435.5; DB 13; Length 300;
Best Local Similarity 34.7%; Pred. No. 3.1e-34;
Matches 103; Conservative 54; Mismatches 115; Indels 25; Gaps 7;

OY 20 LLLIFRGLIGAV---NIKSNRTFVVOEFSEVELSCIITDSDSD---PRIEMWKIODE 73
DB 23 LALLCCCLMTNALAGVTAAPPTITVYEGDSFDLR-----SYSDIYNPRVEMKFPVAKDQ 78
OY 74 OTTVFPFNKIQGDLAGEAELIGKTSLKINWTRBDALYRCEVANDRKEIDEIVIEL 133
```

DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Junction cell adhesion molecule 2.
 GN JAM2 OR JCAM2 (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SKIN;
 RX MEDLINE=22354683; PubMed=22466851;
 RA the FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 DR EMBL: AK028757; BAC26102.1; -
 DR MCD; MGI:1933820; Jam2.
 DR InterPro: IPR003599; IG_1.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 SQ SEQUENCE 298 AA; 33079 MW; C8227EC13D349A3 CRC64;
 Query Match 29.3%; Score 478.5; DB 11; Length 298;
 Best Local Similarity 36.3%; Pred. No. 1.8e-36;
 Matches 113; Conservative 54; Mismatches 117; Indels 27; Gaps 9;
 QY 13 ARDPFLLLPFRGLIAVNLKSSN-----RPPVQEFSEVLSCTIDSDPRFEMKIDDEQ 63
 DB 2 ARSPQGLMLLHLVLYALDYHAKNGFSASKRQEVLTIEPEALILAC-KTPKKTSS 60
 QY 64 RIEMKKIQDEQTYVFNKIQGLAGRAELIGKTSLKIMWTRRDSALYRCEVYARNDRE 123
 DB 61 RLEWKV-GQGVSLVYVQALQGFEDKDAEMI-DFNIRIKVTHSDAGEVCEVAPTEQ 118
 QY 124 -KEIDVIELTVQYKVPVCRVPKAVPVGMATLHQSESGHPRHYSWYNDVPLPT 182
 DB 119 GQNLQEDKYLEVLMAPVAPFACEVPTSVMTGSVELRCQDKEGNPAPETIWFKDG---T 174
 QY 183 DSRAMP---FRNSSHLSSETGLVFTAVHKDSDGQYCIASNDAGSARCEQEMEYVD 239
 DB 175 SLGNPKGKTNNSSYTMATKSGIIQFNKISMDSGEYCEARNSVGHRRPGKRMQVDV 234
 QY 240 INIGGIIGVVLVAVLALITLIGICAVRGGFIINNKDGSYSYKPGKPDGVNTRIDEE 299
 DB 235 INISGIIAVVVAVFVSVCGIGTCYAKRGYF-----SKETSFQKSP--ASKVTIWE 287
 QY 300 GDFRKSSFVI 310
 DB 288 NDFKHKTSFTI 298
 RESULT 10
 Q9JHY1 PRELIMINARY; PRT; 300 AA.
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Junctional adhesion molecule JAM.
 GN JAM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley;
 RA Mashima H., Kojima I.;
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF276998; AAF78250.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 SQ SEQUENCE 300 AA; 32369 MW; 45AB362A96158BFA CRC64;
 Query Match 28.0%; Score 458.5; DB 11; Length 300;
 Best Local Similarity 37.9%; Pred. No. 1.7e-36;
 Matches 113; Conservative 48; Mismatches 122; Indels 15; Gaps 8;
 QY 20 LLLPFRGLIA-VNLKSNRTP---VQGFSEVLSCTIDSDPRFEMKIDDEQ 74
 DB 11 LILFETSMILSLVQKGSVYSPQAVQVENDSVKLPCLY--SGFSRPRVEMKIFVQGST 68
 QY 75 TTYVFPDNKIQGLAGRAELIGKTSLKIMWTRRDSALYRCEVYARNDREKIDEIVIELT 134
 DB 69 TALVCTNNQITVPYADRY-TSSSGITFSSVTRKDNGBYT-C-MVSEDGQVYGEVSIHLT 126
 QY 135 VQKVPVTPVCRVPKAVPVGMATLHQSESGHPRHYSWYNDVPLPT-DSRAMPFRNS 193
 DB 127 VLVPPSKPTVSISSSVITGNRAVLTCSEHDSPPSEYSWFKDGVPMLTADKKTRAFINS 186
 QY 194 SSHLSSETGLVFTAVHKDSDGQYCIASNDAGSA-RCEQEMEYVDINIGIIGVLYV 252
 DB 187 STTIPKSGDLVDFDVSAFDSGEYCEANQNGVGTMRSEAVRMEVNLVNGIVAAVLVT 246
 QY 253 LAVALITLIGICAVRGGFIINNKDGSYSYKPGKPDGVNTRIDEE DPFKSSFVI 310
 DB 247 LILGLIFGIWFAVSRGYFERTKKG---TAPGKVIYSOPARSBEFQOTSSFLV 300
 RESULT 11
 Q7ZWTO PRELIMINARY; PRT; 289 AA.
 AC Q7ZWTO;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Similar to junctional adhesion molecule 1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC046720; AAH46720.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003598; IG_C2.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00408; IGC2; 2.
 DR PROSITE: PS50835; IG_LIKE; 2.
 SQ SEQUENCE 289 AA; 31630 MW; 24354BSA37618845 CRC64;
 Query Match 27.8%; Score 455; DB 13; Length 289;
 Best Local Similarity 35.8%; Pred. No. 3.6e-36;
 Matches 103; Conservative 56; Mismatches 109; Indels 20; Gaps 7;
 QY 27 CLIGAVNL---KSNRTPVVQEFSEVLSCTIDSDPRFEMKIDDEQ 82
 DB 18 CCLWTVTLAAVTPNPITIVKESASALQCSYSSDFTS-PRVMEKRVNKOETSFVFDYD 76

RC STRAIN=C57BL/6J; PubMed=10779521;
 RA MEDLINE=20317114; PubMed=10779521;
 RA Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
 RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of
 the Immunoglobulin Superfamily, is Localized to InterCellular
 Boundaries of Endothelial Cells";
 RA J. Biol. Chem. 275:19139-19145(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=11036763;
 RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
 RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
 Family?";
 RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Irawa M., Nishi K., Kiyosawa H., Kamoto S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojohori T., Sono H., Kasukawa T., Saito R.,
 RA Kaotora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Flieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita W., Gariboldi M.,
 RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima M., Mazzaletti J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AF255911; AAF81224.1; -;
 DR EMBL; AJ291757; CAC20699.1; -;
 DR EMBL; AK013914; BAB29053.1; -;
 DR EMBL; AK010616; BAB27064.1; -;
 DR MGD; MGI:1933820; Jam2; -;
 DR InterPro: IPR007110; IG-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;
 Query Match 29.4%; Score 481.5; DB 11; Length 298;
 Best Local Similarity 36.7%; Pred. No. 9.3e-39;
 Matches 114; Conservative 53; Mismatches 117; Indels 27; Gaps 9;
 QY 13 ARLPDFLLLFRCGLIGAVNLKSSN-----RTPVQEFSEVELSCITTSQSDP 63
 DB 2 ARSPQGLMLLHLVLAIDYHANGFSASKDRQEVTVIEFOEAILAC-KTRPKTTSS 60
 QY 64 RIEMKKIODEQTYVFPDNKIQGLDLAGRAELIGKTSIKINVTTRDSALYRCEVVAANDR 123
 DB 61 RLEWKKYV-GQGVSVLYVYQALQGFDFKRAEMI-DENIRIKNVTSDAGEYCEVSAPTEQ 118
 QY 124 -KEIDEIVIELTVQVKEVTPVCEVPAVPGKATLHCQSESEGHPRPHSYTRNDVPLEPT 182
 DB 119 GQNLQEDKVMLEVLVAAPVACEVPTSVMTGVSVELRCQDEGNPAPEYIMFKGHSI-- 174
 QY 183 DSRANPR---FRSSSHINSEGTIVFTAVHKDSDGQYCIASNDAGARCEQEMEYVD 239
 DB 175 SLIGNFKGTHNNSSYTMNTKSGILGFNMISKDSDGEYCEARNVGHRRCPGKRMQVDV 234
 QY 240 LNIIGIIGVLYVLAVLALITLIGICCAVRRGYFINNKQDGEYSYKPNKPGVNYIRTDDE 299
 DB 235 LNIIGIATVVVAFAVISVGLGTCVAKRGYF-----SKETSFQKSP--ASKVTITMSE 287
 QY 300 GDFRHKSSFYI 310

DB 288 NDFPKTKSFII 298
 RESULT 8
 Q8CEK9 PRELIMINARY; PRT; 298 AA.
 ID Q8CEK9
 AC Q8CEK9
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Junction cell adhesion molecule 2.
 GN JAM2 OR UCAM2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12468851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK078128; BAC37139.1; -;
 DR MGD; MGI:1933820; Jam2.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG-C2.
 DR InterPro: IPR003596; IG-V.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SMO0409; IG; 2.
 DR SMART; SMO0408; IGV; 1.
 DR SMART; SMO0406; IGV; 2.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 SQ SEQUENCE 298 AA; 33182 MW; 1131F0BF89CEB51 CRC64;
 Query Match 29.4%; Score 481.5; DB 11; Length 298;
 Best Local Similarity 37.0%; Pred. No. 9.3e-39;
 Matches 115; Conservative 53; Mismatches 116; Indels 27; Gaps 9;
 QY 13 ARLPDFLLLFRCGLIGAVNLKSSN-----RTPVQEFSEVELSCITTSQSDP 63
 DB 2 ARSPQGLMLLHLVLAIDYHANGFSASKDRQEVTVIEFOEAILAC-KTRPKTTSS 60
 QY 64 RIEMKKIODEQTYVFPDNKIQGLDLAGRAELIGKTSIKINVTTRDSALYRCEVVAANDR 123
 DB 61 RLEWKKYV-GQGVSVLYVYQALQGFDFKRAEMI-DENIRIKNVTSDAGEYCEVSAPTEQ 118
 QY 124 -KEIDEIVIELTVQVKEVTPVCEVPAVPGKATLHCQSESEGHPRPHSYTRNDVPLEPT 182
 DB 119 GQNLQEDKVMLEVLVAAPVACEVPTSVMTGVSVELRCQDEGNPAPEYIMFKGHSI-- 176
 QY 183 DSRANPR---FRSSSHINSEGTIVFTAVHKDSDGQYCIASNDAGARCEQEMEYVD 239
 DB 177 -LGNPKRTHNNSSYTMNTKSGILGFNMISKDSDGEYCEARNVGHRRCPGKRMQVDV 234
 QY 240 LNIIGIIGVLYVLAVLALITLIGICCAVRRGYFINNKQDGEYSYKPNKPGVNYIRTDDE 299
 DB 235 LNIIGIATVVVAFAVISVGLGTCVAKRGYF-----SKETSFQKSP--ASKVTITMSE 287
 QY 300 GDFRHKSSFYI 310
 DB 288 NDFPKTKSFII 298
 RESULT 9
 Q8CE95 PRELIMINARY; PRT; 298 AA.
 ID Q8CE95
 AC Q8CE95
 DT 01-MAR-2003 (TREMblrel. 23, Created)

RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strassberg R.;
 RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=mesonephros;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).

DR EMBL; AJ30304; CAC20704.1; -
 DR EMBL; AK013156; BAB28683.1; -
 DR EMBL; BC024357; AAB24357.1; -
 DR EMBL; AK032833; BAC28049.1; -
 DR MGD; MGI:1933825; Jam3.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IgC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 86.5%; Score 1415; DB 11; Length 310;
 Best Local Similarity 86.1%; Pred. No. 1.6e-130;
 Matches 267; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLLRGCLIGAVNLKSSNRTPVVOEFSEVLSCTITDSQT 60
 DB 1 MALRRRLRLRYARLPDFLLLRGCMIEKVNKSNRPVVEFSEVLSCTITDSQT 60

QY 61 SDPRLEWKKIQDEQTTVFFPNKIQGDLAAGTDFGKTSLRIMVTRDSALYRCEVVAL 120
 DB 61 SDPRLEWKKIQDGGTTVFFPNKIQGDLAAGTDFGKTSLRIMVTRDSALYRCEVVAL 120

QY 121 NDRKEIDEIVIELTVQVKEVTPVCRVPAVPGKATLHCQESGHPHPSWYRNDVPL 180
 DB 121 NDRKEVEDEITIELIVQVKEVTPVCRIPAVPGKATLHCQESGHPHPSWYRNDVPL 180

QY 181 PTDSRANPRFNSSSHLNSGTIVFTAVHKDSCGYCIASNDGASARCEQMEVYDL 240
 DB 181 PTDSRANPRFNSSSHNSGTIVFTAVHKDSCGYCIASNDGASARCEQMEVYDL 240

QY 241 NIAGIIGVLLVLAVALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDSEG 300
 DB 241 NIAGIIGVLLVLAVALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDSEG 300

QY 301 DFRHKSFEVI 310
 DB 301 DFRHKSFEVI 310

RESULT 6
 Q9D1M9 PRELIMINARY; PRT; 310 AA.
 AC Q9D1M9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE 111002N23Rik protein.
 GN JCAM3 OR JCAM2 OR 111002N23Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeble G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Mommaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz K.H., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kottewski S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK003326; BAB22715.1; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IgC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 85.8%; Score 1403; DB 11; Length 310;
 Best Local Similarity 85.2%; Pred. No. 2.5e-129;
 Matches 264; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLLRGCLIGAVNLKSSNRTPVVOEFSEVLSCTITDSQT 60
 DB 1 MALSRRLRLRYARLPDFLLLRGCMIEKVNKSNRPVVEFSEVLSCTITDSQT 60

QY 61 SDPRLEWKKIQDEQTTVFFPNKIQGDLAAGTDFGKTSLRIMVTRDSALYRCEVVAL 120
 DB 61 SDPRLEWKKIQDGGTTVFFPNKIQGDLAAGTDFGKTSLRIMVTRDSALYRCEVVAL 120

QY 121 NDRKEIDEIVIELTVQVKEVTPVCRVPAVPGKATLHCQESGHPHPSWYRNDVPL 180
 DB 121 NDRKEVEDEITIELIVQVKEVTPVCRIPAVPGKATLHCQESGHPHPSWYRNDVPL 180

QY 181 PTDSRANPRFNSSSHLNSGTIVFTAVHKDSCGYCIASNDGASARCEQMEVYDL 240
 DB 181 PTDSRANPRFNSSSHNSGTIVFTAVHKDSCGYCIASNDGASARCEQMEVYDL 240

QY 241 NIAGIIGVLLVLAVALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDSEG 300
 DB 241 NIAGIIGVLLVLAVALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDSEG 300

QY 301 DFRHKSFEVI 310
 DB 301 DFRHKSFEVI 310

RESULT 7
 Q9J1S9 PRELIMINARY; PRT; 298 AA.
 AC Q9J1S9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Vascular endothelial junction-associated molecule (functional adhesion
 DE molecule-3) (241030G21Rik protein).
 GN JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 241030G21Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN SEQUENCE FROM N.A.

QY	2	ALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOFBSVLSCTITTSQTS	61
DB	1	ALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOFBSVLSCTITTSQTS	60
QY	62	DPRIEMWKIDQEQTYTFYFNDKIQGDLGAEILGKTLKIMVTRDSALYCEVVAR	121
DB	61	DPRIEMWKIDQEQTYTFYFNDKIQGDLGAEILGKTLKIMVTRDSALYCEVVAR	120
QY	122	DRKREIDIVELTYQKVPVPCRVPAVGVKATLHCQESGHPHYSWYRNDVPLP	181
DB	121	DRKREIDIVELTYQKVPVPCRVPAVGVKATLHCQESGHPHYSWYRNDVPLP	180
QY	182	TDRRANFRFNSSSHNSETGTLVFTAVHDKDSGOYYCIASNDAGARCEQMEVYDL	241
DB	181	TDRRANFRFNSSSHNSETGTLVFTAVHDKDSGOYYCIASNDAGARCEQMEVYDL	240
QY	242	IGGIIGGVVLLVAVLALITGICAYRGGYFINKKDGESYKPKGPDGVNYIRTDSEG	301
DB	241	IGGIIGGVVLLVAVLALITGICAYRGGYFINKKDGESYKPKGPDGVNYIRTDSEG	300
QY	302	FRHKSSFVI 310	
DB	301	FRHKSSFVI 309	

RESULT 4
Q9DB87 PRELIMINARY; PRT; 310 AA.

Q9DB87
AC Q9DB87
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE 1110002N23R1K protein.
JCAM3 OR JCAM2 OR 1110002N23R1K.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Small Intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai U., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuent P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake U., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.U., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK008187; BAB2519.1;
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00408; IgC2; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 3485 MW; C74884FAB234680 CRC64;

Query Match 86.7%; Score 1417; DB 11; Length 310;
Best Local Similarity 86.1%; Pred. No. 1e-150;

	Matches	267; Conservative	19; Mismatches	24; Indels	0; Gaps	0;
QY	1	MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOFBSVLSCTITTSQTS	60			
DB	1	MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOFBSVLSCTITTSQTS	60			
QY	61	SDPRIEMWKIDQEQTYTFYFNDKIQGDLGAEILGKTLKIMVTRDSALYCEVVAR	120			
DB	61	SDPRIEMWKIDQEQTYTFYFNDKIQGDLGAEILGKTLKIMVTRDSALYCEVVAL	120			
QY	121	NDRKREIDIVELTYQKVPVPCRVPAVGVKATLHCQESGHPHYSWYRNDVPL	180			
DB	121	NDRKREIDIVELTYQKVPVPCRVPAVGVKATLHCQESGHPHYSWYRNDVPL	180			
QY	181	PTDSRANFRFNSSSHNSETGTLVFTAVHDKDSGOYYCIASNDAGARCEQMEVYDL	240			
DB	181	PTDSRANFRFNSSSHNSETGTLVFTAVHDKDSGOYYCIASNDAGARCEQMEVYDL	240			
QY	241	NIGGIIGGVVLLVAVLALITGICAYRGGYFINKKDGESYKPKGPDGVNYIRTDSEG	300			
DB	241	NIGGIIGGVVLLVAVLALITGICAYRGGYFINKKDGESYKPKGPDGVNYIRTDSEG	300			
QY	301	DEPRKSSFVI 310				
DB	301	DEPRKSSFVI 310				

RESULT 5
Q9EPK4 PRELIMINARY; PRT; 310 AA.

Q9EPK4
AC Q9EPK4
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23R1K protein)
(Junctional cell adhesion molecule 3).
JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23R1K.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP PubMed=11036763;
RX Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
[2]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai U., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuent P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake U., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.U., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]

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OW protein - protein search, using sw model

Run on: April 12, 2004, 09:12:08 ; Search time 45 Seconds
(without alignments)

2173.570 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 1635
Sequence: 1 MALRRPRLRLCARLPDFLL.....VNYIRDEGDFRRKSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1629	99.6	310	4 Q9BX67	Q9BX67 homo sapien
2	1629	99.6	355	4 Q8WML8	Q8WML8 homo sapien
3	1620	99.1	309	4 Q96FL1	Q96FL1 homo sapien
4	1417	86.7	310	11 Q9B5B7	Q9B5B7 mus musculu
5	1415	86.5	310	11 Q9B5B7	Q9B5B7 mus musculu
6	1403	85.8	310	11 Q9D1M9	Q9D1M9 mus musculu
7	481.5	29.4	298	11 Q9C1S9	Q9C1S9 mus musculu
8	481.5	29.4	298	11 Q8C5K9	Q8C5K9 mus musculu
9	478.5	29.3	298	11 Q8C5K9	Q8C5K9 mus musculu
10	458.5	28.0	300	11 Q9JHY1	Q9JHY1 rattus norv
11	455	27.8	289	13 Q7ZWT0	Q7ZWT0 xenopus lae
12	449.5	27.5	300	11 Q8YC39	Q8YC39 mus musculu
13	435.5	26.6	300	13 Q7SYQ7	Q7SYQ7 xenopus lae
14	331	20.2	259	4 Q9Y5B2	Q9Y5B2 homo sapien
15	321	19.6	173	11 Q9JYD5	Q9JYD5 rattus norv
16	291	17.8	64	11 Q8BT59	Q8BT59 mus musculu

17	248	15.2	318	13 Q91664	Q91664 xenopus lae
18	242.5	14.8	304	11 Q9CVA4	Q9CVA4 mus musculu
19	241	14.7	307	4 Q96I07	Q96I07 homo sapien
20	239.5	14.6	284	4 Q9N442	Q9N442 homo sapien
21	238.5	14.6	325	4 Q85791	Q85791 mus musculu
22	232.5	14.2	328	11 Q9Z109	Q9Z109 mus musculu
23	221.5	13.5	319	11 Q9Z2D5	Q9Z2D5 mus musculu
24	215.5	13.2	319	11 Q9JKA5	Q9JKA5 mus musculu
25	215	13.1	407	11 Q9D2J4	Q9D2J4 mus musculu
26	209.5	12.8	335	13 Q9PWR4	Q9PWR4 gallus gall
27	209	12.8	181	13 Q91665	Q91665 xenopus lae
28	206.5	12.6	335	13 Q9YGH1	Q9YGH1 gallus gall
29	205.5	12.6	248	11 Q9D0T4	Q9D0T4 mus musculu
30	201.5	12.3	335	13 Q9YGV5	Q9YGV5 gallus gall
31	199.5	12.2	332	13 Q9YV50	Q9YV50 brachydario
32	198.5	12.1	387	4 Q86XK7	Q86XK7 homo sapien
33	197.5	12.1	373	4 Q9H6B4	Q9H6B4 homo sapien
34	193.5	11.8	735	13 Q9OYMO	Q9OYMO brachydario
35	189	11.6	259	4 Q7Z2C1	Q7Z2C1 homo sapien
36	187	11.4	725	13 Q73633	Q73633 xenopus lae
37	186.5	11.4	338	13 Q90490	Q90490 brachydario
38	184.5	11.3	372	11 Q90YM1	Q90YM1 brachydario
39	182.5	11.2	372	11 Q8X1G0	Q8X1G0 rattus norv
40	182.5	11.2	1409	13 Q8J127	Q8J127 brachydario
41	182.5	11.2	1409	13 Q801M2	Q801M2 brachydario
42	182.5	11.2	1428	13 Q8AY67	Q8AY67 brachydario
43	180.5	11.0	1894	11 Q64487	Q64487 mus musculu
44	180	11.0	344	5 Q8WR42	Q8WR42 caenorhabdi
45	180	11.0	345	5 Q8MPV0	Q8MPV0 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q9BX67	PRELIMINARY;	PRT;	310 AA.
AC	Q9BX67;			
DT	01-JUN-2001 (TREMBL)	17, Last sequence update)		
DT	01-JUN-2001 (TREMBL)	17, Last sequence update)		
DT	01-OCT-2003 (TREMBL)	25, Last annotation update)		
DE	Functional adhesion molecule 3 precursor (functional adhesion molecule-2) (functional adhesion molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90828).			
DE	JAM-2 OR JAM3.			
GN	JAM-2 OR JAM3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Cunningham S.A., Arrate M.P., Tran T.M.;			
RT	"Cloning of Human Junctional Adhesion Molecule 3";			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Aurand-Lions M.A., Johnson-Jeger C., Wong C., Dupasquier L.;			
RT	"Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Aurand-Lions M.A., Johnson-Jeger C., Lamagna C., Ozaki H., Kita T.;			
RT	"Functional adhesion molecules (JAMs) and interendothelial junctions";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Sachs U.U.H., Eva O., Berghofer H., Santoso S.;			
RT	"Characterization of Junctional Adhesion Molecule-3 on Human Platelets. A New Member of Immunoglobulin Superfamily";			

DR HSP, P12931, 1FMK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig_7.
DR Pfam; PF00069; kinase_1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0408; IGC2; 4.
DR SMART; SMO0219; TYKC; 1.
DR PROSITE; PSS0835; IG_Like; 7.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PSS0109; PROTEIN_KINASE_TYR; 1.
DR Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 22
FT CHAIN 23 1051
FT DOMAIN 23 685
FT TRANSMEM 686 706
FT DOMAIN 707 1051
FT DOMAIN 23 105
FT DOMAIN 115 204
FT DOMAIN 213 298
FT DOMAIN 308 388
FT DOMAIN 393 472
FT DOMAIN 487 566
FT DOMAIN 573 661
FT DOMAIN 777 1048
FT DISULFID 40 88
FT DISULFID 137 187
FT DISULFID 234 282
FT DISULFID 326 372
FT DISULFID 414 462
FT DISULFID 505 551
FT DISULFID 594 645
FT CARBOHYD 103 103
FT CARBOHYD 202 202
FT CARBOHYD 255 255
FT CARBOHYD 264 264
FT CARBOHYD 444 444
FT CARBOHYD 548 548
FT CARBOHYD 627 627
SQ SEQUENCE 1051 AA; 116366 MW; 1752442EA4CB702 CRC64;

Query Match 10.1%; Score 164.5; DB 1; Length 1051;
Best Local Similarity 24.5%; Pred. No. 6.9e-06;
Matches 66; Conservative 35; Mismatches 109; Indels 59; Gaps 11;

QY 40 TPVVQEFSEVE-----LSCLITDSQTSDPRIEMKKIQDEQTYVFFDNKIQGDLAAR 93
DB 486 TPPQPPQCEKFEKVTSCSARGE--KPTQMTKD-----GSLPSHVSRRAG 534
QY 94 ILGKTSIKINVTFRSDALYRCEVVAARDKEIDEIVELTVQKPTVPCRVKAVPVG 153
DB 535 I-----LSFKVSRSDSGNTCC--IASNSPQGEIRATVQLVAVVYTPKLEPEFTVYG 587
QY 154 KMATLHQESEGHPRPYSYRNDVPLPTSRANPRFRNSSHLNSETGLVFTAVHKDD 213
DB 588 HTLMFQCC-AEGDFVPHIQWGRKDL-DPSKLPRIQMPN-----GSLVYDVTTSD 639
QY 214 SGQYYCIASNDAG-----SARCEQE-----MEVYDLNIGIIGVLY 251
DB 640 SGKTYCTIAGNSCNKIKREAFLYVVDKPALEDDEGSSHTPYKMIQTIGLSVGAAYVIII 699
QY 252 VLAVLAILITIGICAYRGRYFINNKQDGE 280
DB 700 VLGLMF-----YCKRRKAKRLKKGPEGE 723

[illegible]

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FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .)
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 837 AA; 92932 MW; C3D04106C5741C1 CRC64;

Query Match 10.1%; Score 165; DB 1; Length 837;
Best Local Similarity 24.3%; Pred. No. 4,7e-06;
Matches 72; Conservative 31; Mismatches 105; Indels 88; Gaps 15;

QY 44 QEF---ESVLSCLITDQSDSPRIEKKIKIQDEQTVVFPDNKIQGLAGRAELIGKSL 100
DB 124 QEFKQSGDAVAVCRVSSSPA--PAVSLVLYNEEYTT--ISDN-----RLAFLANNLT 171
QY 101 KIMVTRRDSALYRCE--VYARNDKREIDELVIELTVQVQVLPVCKVPKAPV----- 152
DB 172 QILNINSDGDIYRCBGRVARGE-----IDRFDIIVVNPAPAIAMPQKSFN 219
QY 153 -----GKATLHCQSESGHPHYSWYRNDVPLPTDSRAPRFRNSSSHUNSEGTIVFT 207
DB 220 ATARGESEMFSCRPAS--GSPEPAISWRNGKLE-----ENEXYILKGSNTLTVR 269
QY 208 AVHKDSGGYYCIASNDASARCEQMEYVDNLGIGLVYVLAVALITIGICAY 267
DB 270 NIINSDGFPVCAATNKAQ-----EDKQAF-----LQVFPQHILQKNETTY 313
QY 268 RRGVFINNKDDGSEKVPKRP-----DGVNVRTDEGDFR-----HKSS 307
DB 314 ENQGVTLVQDAE-----GEPPIETMKRAVDGFTFEGSKSPGRLEVKQGHSS 363

RESULT 15
PRT7_CHICK STANDARD; PRT; 1051 AA.
AC Q91048;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DS Tyrosine-protein kinase-like 7 precursor (kinase like protein) .
GN PTK7 OR KLG.
OS Gallus gallus (chicken) .
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxId=9031;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic brain;
RX MEDLINE=91271300; PubMed=1711213;
RA Chou Y.-H., Hayman M.J.;
RT "Characterization of a member of the immunoglobulin gene superfamily
RT that possibly represents an additional class of growth factor
RT receptor.";
RL Proc Natl. Acad. Sci. U.S.A. 89:4987-4991(1992).
CC -1- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
CC THE CATALYTIC ACTIVITY OF TYROSINE KINASE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA,
CC THYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLASTS. ALSO EXPRESSED
CC IN EMBRYONIC LIVER.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
EMBL, M63437, AAA48933.1; -.
PIR, A39712; A39712.

```

Mammalia; Eutheria; Primates; Carnivora; Homini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
 MEDLINE=95204468; PubMed=7896816;
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
 "Molecular characterization of the human transmembrane protein-
 tyrosine phosphatase delta. Evidence for tissue-specific expression of
 alternative human transmembrane protein-tyrosine phosphatase delta
 isoforms.";
 J. Biol. Chem. 270:6722-6728 (1995).
 [2]
 SEQUENCE OF 390-1912 FROM N.A.
 TISSUE=Placenta;
 MEDLINE=91006018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.;
 "Structural diversity and evolution of human receptor-like protein
 tyrosine phosphatases.";
 EMBO J. 9:3241-3252 (1990).
 -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 -1- SUBCELLULAR LOCATION: Type I membrane protein.
 -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=3;
 Comment=Additional isoforms seem to exist;
 Name=1;
 IsoId=P23468-1; Sequence=Displayed;
 Name=2; Synonyms=Kidney;
 IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
 Name=3; Synonyms=Petal brain;
 IsoId=P23468-3; Sequence=VSP_005150;
 -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 FROM THE TRANSMEMBRANE SEGMENT.
 -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 -1- SIMILARITY: Contains 8 fibronectin type III domains.
 -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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 CC
 CC EMBL; L38929; AAC41749.1; -
 CC EMBL; X54133; CAA38068.1; -
 CC PIR; A56178; A56178.
 CC HSSP; P18052; IYFO.
 DR Genew; HGNC:9666; PTPRD.
 DR MIM; 601598; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.
 DR GO; GO:0006470; P:protein amino acid phosphorylation; TAS.
 DR GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. .; TAS.
 DR InterPro; IPR006957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PR00041; fn3; 8.
 DR Pfam; PR00047; IG_3.
 DR Pfam; PR00102; Y_phosphatase; 2.
 DR PRINTS; PR00014; FNTYPIII.
 DR PRINTS; PR00700; PRTYPIIIASE.
 DR SMART; SM00060; FN3; 8.
 DR SMART; SM00408; IGc2; 2.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PSS0835; IG_LIKE; 3.
 DR PROSITE; PSS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS00383; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PSS00056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 1912
 FT DOMAIN 21 1265
 FT TRANSMEM 1266 1290
 FT DOMAIN 1291 1912
 FT DOMAIN 24 114
 FT DOMAIN 126 224
 FT DOMAIN 236 318
 FT DOMAIN 320 414
 FT DOMAIN 417 513
 FT DOMAIN 516 606
 FT DOMAIN 609 708
 FT DOMAIN 711 822
 FT DOMAIN 825 916
 FT DOMAIN 918 1017
 FT DOMAIN 1020 1137
 FT DOMAIN 1375 1618
 FT DOMAIN 1619 1912
 FT ACT_SITE 1553 1553
 FT ACT_SITE 1844 1844
 FT SITE 1175 1178
 FT CARBOHYD 254 254
 FT CARBOHYD 299 299
 FT CARBOHYD 724 724
 FT CARBOHYD 832 832
 FT VASAPLIC 181 189
 FT VASAPLIC 226 229
 FT VASAPLIC 775 783
 FT VASAPLIC 609 1137
 FT MUTAGEN 1178 1178
 FT SEQUENCE 1912 AA; 214759 MW; 3AB8C8D32182E26 CRC64;
 SQ
 Query Match 10.4%; Score 169.5; DB 1; Length 1912;
 Best Local Similarity 28.6%; Pred. No. 5.6e-06;
 Matches 65; Conservative 35; Mismatches 76; Indels 51; Gaps 13;
 QY 39 RTPVQEFSEVLESCITTDSDPFR-IEW-----KKIQDQTYVFFDNKIQGDLAGRA 92
 DB 28 RTPVDQGVSGVASFICQA-TGDPFRKIVNNKKGKVSQREVEIFED-----GSG 79
 QY 93 EILKTSIKIWNVTRDSALYRCGVARNRKEIDELVILTYQKAVTVGVCKVXPV 152
 DB 80 SVLRICQPLR-----TPRDEALYEC--VASNNVGEI-SVSTRLTYLRBD-----QIPRGFT 127
 QY 153 GK-----ATLHCSESGHPRPHYSVRNDVPLPTDSRANPRFNSSSHLNS 200
 DB 128 IDKMPQLKVVERTATMLCAAS-GNPDEITWIKDLPVDT-SNNNGRIK-----QLRSE 181
 QY 201 T-----GTLVFTFAVHKDSGGQYICIASDAGARCEQSEMEVYDL 240
 DB 182 SIGGPIRGALQIQSESESDQKTECVATNSAGTRVAPANLYREL 228
 RESULT 14
 NCNM2 HUMAN STANDARD; PRT; 837 AA.
 ID NCNM2 HUMAN
 AC O15394;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neutral cell adhesion molecule 2 precursor (N-CAM 2).
 GN NCNM2 OR NCAM21.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Best Local Similarity 31.0%; Pred. No. 2.8e-06;
Matches 61; Conservative 21; Mismatches 69; Indels 46; Gaps 9;

QY 47 ESVELSCITTSQTSQDPRLEWKKIDDEQTYVFFDNKIQGLAGRAELIGKTSKIMVVT 106
DB 233 QSAVLPCTVA--SGLEPAPIRMKMKEDVDT-----ESSGRLALLAGSLEISVT 280
QY 107 RSDSALYRCEVVAARDKREIDELVIELTVQYKPTPVCRVPAVFGKMATLHQES-- 163
DB 281 EDDAGTYFC--VADGNKNTI--SAQALTYQVPPPE-----LKQPAIVYARESMDI 327
QY 164 -----EGHPRPHYSWYRN-DYPLPTDSRANRPNSSSHLNSERTGLVFAVHKDDSGQ 216
DB 328 VECVETGKPAFTVKKVNGDVVIFSD-----YFKIVKH-----NLQVGLVKSDEGF 376

QY 217 YYCIASNDAGSARCEQ 233
DB 377 YOCIAENDVGNAGAGQ 393

RESULT 12
NCAL RAT
ID NCAL RAT STANDARD; PRT; 858 AA.
AC P13596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (NCAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=8059265; PubMed=3680385;
RA Small S.J., Shull G.E., Santoni M.-J., Akeson R.;
RT Identification of a cDNA clone that contains the complete coding
sequence for a 140-kD rat NCAM polypeptide.";
RL U. Cell Biol. 103:2335-2345(1987).
RN [2]
RP SEQUENCE OF 355-364 FROM N.A.
RX MEDLINE=90166485; PubMed=2483093;
RA Small S.J., Haines S.L., Akeson R.A.;
RT Polypeptide variation in an N-CAM extracellular immunoglobulin-like
fold is developmentally regulated through alternative splicing.";
RL Neuron 1:1007-1017(1988).
CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
neuron-neuron adhesion, neurite fasciculation, outgrowth of
neurites, etc.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P13596-1; Sequence=Displayed;
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
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CC EMBL: X06564; CAA29809.1; -;
CC EMBL: M32611; AAA1679.1; -;
CC PIR: S00846; IRTNC.
CC DR PDB: 1BPP; 27-OCT-00.

DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PRF00041; fn3; 2.
DR Pfam; PRF00047; Ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IgC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
KW 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 858
FT FT
FT DOMAIN 20 721
FT TRANSMEM 722 739
FT DOMAIN 740 858
FT DOMAIN 20 111
FT DOMAIN 116 205
FT DOMAIN 212 302
FT DOMAIN 309 414
FT DOMAIN 417 502
FT DOMAIN 514 615
FT DOMAIN 616 712
FT DOMAIN 152 156
FT DOMAIN 161 165
FT DISULFID 41 96
FT DISULFID 139 189
FT DISULFID 235 288
FT DISULFID 330 396
FT DISULFID 437 490
FT CARBOHYD 422 222
FT CARBOHYD 316 316
FT CARBOHYD 348 348
FT CARBOHYD 434 434
FT CARBOHYD 460 460
FT CARBOHYD 489 489
SQ SEQUENCE 858 AA; 94658 MW; EAL064AE050F6 CRC64;
Query Match 10.4%; Score 170.5; DB 1; Length 858;
Best Local Similarity 26.3%; Pred. No. 1.7e-06;
Matches 61; Conservative 41; Mismatches 85; Indels 45; Gaps 12;

QY 27 CLTGA-----VNLKSNR-----TPVQEFSEVLSCTITDSQTS-DPRLEWKKIQ 71
DB 96 CVTALEPGTQSEATVNVKIRQKMPKPAFPQSEKGEADAVIYODVVSILPFLTK-- 152
QY 72 DEQTYVFPDNKIQGLAGRAELIGKTSKIMVTRDSALYCE--VVARNDKREIDEI 129
DB 153 -----HKGRAVILKKDV--RFIVLSNNYLDIRGIKKTDEGTYRCEGRILRG---ELNFK 202
QY 130 VIELTVQKPTVPCR--VEKAVPGKMATLHQESGHPHRYSWRNDVPLPTDSRAN 187
DB 203 DQIVTVNPPPTVQARQSVIVATNLTGSGVTLVC-DADGFEPHMSWKQDEPLENEB--- 258
QY 188 PRFNSSSH--NSETGLVFTVAVHKDDSGQYYCIASNDAGSARCEDEMEVY 238
DB 259 ---EDKEHIFSDSELTIRNDVKDDEAYVCIANKAG---EDDASIH 302

RESULT 13
PRPD_HUMAN
ID PRPD_HUMAN STANDARD; PRT; 1912 AA.
AC P23468;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
delta).
GN PTPRD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; fn3; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IGc2; 5.
 DR PROSITE; PS50835; IG_1like; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 DR Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
 KW SIGNAL
 FT CHAIN 1 19
 FT 20 115 NEURAL CELL ADHESION MOLECULE 1, 180 KDa
 FT 20 115 ISOPROPM
 FT DOMAIN 20 711 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 712 729 POTENTIAL.
 FT DOMAIN 730 1115 CYTOPLASMIC (POTENTIAL).
 FT 20 111 IG-LIKE C2-TYPE 1.
 FT DOMAIN 205 205 IG-LIKE C2-TYPE 2.
 FT 212 302 IG-LIKE C2-TYPE 3.
 FT 309 402 IG-LIKE C2-TYPE 4.
 FT 407 492 IG-LIKE C2-TYPE 5.
 FT 519 596 FIBRONECTIN TYPE-III 1.
 FT 625 692 FIBRONECTIN TYPE-III 2.
 FT 152 156 HEPARIN-BINDING (POTENTIAL).
 FT 161 165 HEPARIN-BINDING (POTENTIAL).
 FT 139 189 PROBABLE.
 FT 235 288 PROBABLE.
 FT 330 386 PROBABLE.
 FT 427 480 PROBABLE.
 FT 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 427 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 479 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 810 1076 Missing (in isoform N-CAM 140).
 FT VARSPLIC
 SQ SEQUENCE 1115 AA; 119351 MW; 2C93DCD474C8BCAF CRC64;
 Query Match 10.5%; Score 171.5; DB 1; Length 1115;
 Best Local Similarity 27.3%; Pred. No. 1.9e-06;
 Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;
 QY 27 CLIGA-----VNLKSSNR-----TPVOPEPSSVELSCITTSQTS-DRIRWKIKIQ 71
 DB 96 CAVTADGQSEATVAVKIFQKIMFKNAPTPQEFKGEBAVAVCVVSLPFTIWK-- 152
 QY 72 DEQTVVFPDNKIQGLDLAGRAELIKTSKIMNWRSDALRCE--VVARDRKEIDEI 129
 DB 153 -----HKGDVILIKV--RFTVLSNNYIQIRGIKTDGTGRCGRILAR--EINPK 202
 QY 130 VIELTVQVPEVTPVCR--VPKAVPVGKATLHCQSESGHPHYMYRNDVLPDTSRAN 187
 DB 203 DIGIVAVPEPTVQARQISVATANTLQSVTLVC-DADGPEPTMSWTXGDEPIENEER-D 260
 QY 188 PRFRNSSHINSETGLTVFAVHKDSSGOYVCASNDASACECEMEVY 238
 DB 261 ERSRSRV---SDSEVTRRNVKNDKDEARVCIANKAG-----EODASIH 302

OX NCBI_TaxID=10116;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97015074; PubMed=8861902;
 RA Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.-Y.,
 RA Culicetti J.G., Tessier-Lavigne M.,
 RT "Deleted in Colorectal Cancer (DCC) encodes a retin receptor."
 RL Cell 87:175-185 (1996).
 CC -1- FUNCTION: May be involved as a regulatory protein in the
 CC transition of undifferentiated proliferating cells to their
 CC differentiated state. May also function as a cell adhesion
 CC molecule in a broad spectrum of embryonic and adult tissues.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. DCC family.
 CC -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 6 fibronectin type III domains.
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 CC -----
 DR EMBL; U68726; AAB41100.1; -.
 DR HSSP; P56276; 1TLX.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00041; fn3; 6.
 DR Pfam; PF00047; fn3; 4.
 DR PRINTS; PR00014; FNTYPEIII.
 DR SMART; SM00060; FN3; 6.
 DR SMART; SM00408; IGc2; 3.
 DR PROSITE; PS50835; IG_1like; 4.
 DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
 KW Glycoprotein.
 FT NON TER 1 1
 FT SIGNAL 2 1377
 FT CHAIN 3 1074
 FT DOMAIN 3 1095
 FT TRANSMEM 1075 1377
 FT 1096 1377
 FT 21 114
 FT 121 206
 FT 198 305
 FT 310 395
 FT 405 502
 FT 505 598
 FT 599 698
 FT 704 798
 FT 819 919
 FT 920 1021
 FT 1087 1090
 FT 142 190
 FT 239 289
 FT 331 379
 FT 42 42
 FT 179 179
 FT 295 295
 FT 439 439
 FT 458 458
 FT 608 608
 FT 684 684
 FT 878 878
 FT 150637 MW; E514ED8ADB1A63A9 CRC64;
 SQ SEQUENCE 1377 AA; 150637 MW; E514ED8ADB1A63A9 CRC64;
 Query Match 10.5%; Score 171; DB 1; Length 1377;
 QY 27 CLIGA-----VNLKSSNR-----TPVOPEPSSVELSCITTSQTS-DRIRWKIKIQ 71
 DB 96 CAVTADGQSEATVAVKIFQKIMFKNAPTPQEFKGEBAVAVCVVSLPFTIWK-- 152
 QY 72 DEQTVVFPDNKIQGLDLAGRAELIKTSKIMNWRSDALRCE--VVARDRKEIDEI 129
 DB 153 -----HKGDVILIKV--RFTVLSNNYIQIRGIKTDGTGRCGRILAR--EINPK 202
 QY 130 VIELTVQVPEVTPVCR--VPKAVPVGKATLHCQSESGHPHYMYRNDVLPDTSRAN 187
 DB 203 DIGIVAVPEPTVQARQISVATANTLQSVTLVC-DADGPEPTMSWTXGDEPIENEER-D 260
 QY 188 PRFRNSSHINSETGLTVFAVHKDSSGOYVCASNDASACECEMEVY 238
 DB 261 ERSRSRV---SDSEVTRRNVKNDKDEARVCIANKAG-----EODASIH 302

RA Giodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalish F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Norris J., Mostrelet A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasmann D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champs M.,
RA George R.A., Garin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A *Drosophila* full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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or send an email to license@isb-sib.ch).
CC EMBL: M23561; AAA28367.1; -;
CC EMBL: AE001572; AAD19797.1; -;
CC EMBL: AE003674; AAF54084.1; -;
CC EMBL: AY051911; AA93335.1; -;
CC PIR: A31923; A31923.
CC FlyBase: FBgn0000071; Ama.
CC GO: GO:0005886; C:plasma membrane; IDA.
CC InterPro: IPR007110; IG_1like.
CC InterPro: IPR003598; IG_C2.
CC Pfam: PF00047; IG_3.
CC SMART: SMO0408; IGc2; 2.
CC PROSITE: PSS0835; IG_1like; 3.
CC Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
KW Repeat.
FT CHAIN 1 23 POTENTIAL.
FT PROPEP ? 333 AMALGAM PROTEIN.
FT DOMAIN 25 128 REMOVED IN NATURE FORM (POTENTIAL).
FT DOMAIN 139 223 IG-LIKE V-TYPE.
FT DOMAIN 230 323 IG-LIKE C2-TYPE 1.
FT DISULFID 46 117 IG-LIKE C2-TYPE 2.
FT DISULFID 161 208 PROBABLE.
FT CARBOHYD 251 307 PROBABLE.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 83 83 Q -> K (IN REF. 1).
SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match 11.0%; Score 180; DB 1; Length 333;
Best Local Similarity 26.8%; Pred. No. 8,2e-08;
Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;
QY 35 KSSNRTPVQEFSEVELSCITTSQSDPRILEMKIDEDQTYFFPNKIQGLAGAEI 94
Db 143 ENTKSTLVEQQLTLC--HANGFPKPTISWR-----ENNAVPAQGH 187
QY 95 LGKSLKIMVTRDSALYRCVAVRNDKREIDVIELTVQVPTVPVCRVPAVEVGK 154
Db 188 LAEPLTIRSVHRMDRGGYC--IAQNGEGQPDRLRIVERPPOIAVQRPKIAQVSH 245
QY 155 MATHCQSESEHPHYSWVRNDVPLETDSRAPRFRNSSSHLNSERTGLVFTAVHDDS 214
Db 246 SAELFC-SVQGYPAFPVWVHKNVPL--QSRHREAVNTASSGQTTSVLRIDVGEEDF 302
QY 215 GQCYCIAANDGSA 228
Db 303 GDYCNATNKLGA 316
RESULT 8
NCA2 XENLA STANDARD; PRT; 1092 AA.
AC P36335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neutral cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE 180).
GN NCAM2.
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93272329; PubMed=7684721;
RA Tonissen K.F., Krieg P.A.;
RT "Two neural-cell adhesion molecule (NCAM)-encoding genes in *Xenopus*
RT laevis are expressed during development and in adult tissues.";
RL Gene 127:243-247(1993).
CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
neuron-neuron adhesion, neurite fasciculation, outgrowth of
neurites, etc.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P36335-1; Sequence=Displayed;
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: M76710; AAA49910.1; -;
CC PIR: UN0635; UN0635.
CC HSBP: P56276; ITLK.
CC InterPro: IPR008957; FN_III-like.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR007110; IG_1like.
CC InterPro: IPR003598; IG_C2.
CC Pfam: PF00041; FN3; 2.
CC Pfam: PF00047; IG; 5.
CC SMART: SMO0060; FN3; 2.

RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
 RT "Primary structure and developmental expression of a large
 cytoplasmic domain form of Xenopus laevis neural cell adhesion
 molecule (NCAM).";
 RL Nucleic Acids Res. 17:10321-10335(1989).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
 neuron-neuron adhesion, neurite fasciculation, outgrowth of
 neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=N-CAM 180;
 CC IsoId=PI6170-1; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=PI6170-2; Sequence=VSP_002589;
 CC -1- TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
 tissue.
 CC -1- DEVELOPMENTAL STAGE: THE mRNA ENCODING THIS LD-NCAM IS THE MAJOR
 TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
 EARLY NEURAL DEVELOPMENT.
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 CC EMBL; M25696; AAA49909.1; -
 DR PIR; S09600; IUXLNL.
 DR HSP; P56276; ITLK.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR003961; FN-III.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SMO0060; FN3; 2.
 DR SMART; SMO0408; IGC2; 5.
 DR POSITIVE; PSS0835; IG Like; 5.
 KM Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KM Immunoglobulin domain; Alternative splicing; Signal.
 KM SIGNAL 1 19
 FT CHAIN 20 1088
 FT
 FT DOMAIN 20 705
 FT TANDSEM 706 723
 FT DOMAIN 724 1088
 FT
 FT DOMAIN 20 108
 FT
 FT DOMAIN 113 202
 FT
 FT DOMAIN 209 294
 FT
 FT DOMAIN 303 397
 FT
 FT DOMAIN 400 484
 FT
 FT DOMAIN 512 589
 FT
 FT DOMAIN 618 686
 FT
 FT DOMAIN 149 153
 FT
 FT DOMAIN 158 162
 FT
 FT DISULFID 41 93
 FT
 FT DISULFID 136 186
 FT
 FT DISULFID 232 282
 FT
 FT DISULFID 323 379
 FT
 FT CARBOHYD 420 473
 FT
 FT CARBOHYD 82 82
 FT
 FT CARBOHYD 219 219
 FT
 FT CARBOHYD 310 310
 FT
 FT CARBOHYD 341 341
 FT
 FT CARBOHYD 417 417
 FT
 FT CARBOHYD 443 443
 FT
 FT CARBOHYD 472 472
 FT
 FT VARSPIC 804 1049
 Missing (in isoform N-CAM 140).

FT
 SQ SEQUENCE 1088 AA; 117778 MM; 6273855803F3E83 CRC64;
 Query Match 11.4%; Score 186; DB 1; Length 1088;
 Best Local Similarity 29.9%; Pred. No. 1,1e-07;
 Matches 63; Conservative 30; Mismatches 82; Indels 36; Gaps 12;
 OY 30 GAVNLK-----SSKRTVQVPEFSEVLSCTITTSQTDPR-IEWK-KIQEQITTVFFDN 82
 DB 105 GTVNLKIYQKLTFRNAFTPEEFKEGEDAVIICDVSSISPIITWRHGXK-----VIFKK 159
 OY 83 KIQGDLGRAEIIIGKTSIKTWNVTRDSALYRGE--VVARND--RKEIDIV-IELTVQV 137
 DB 160 DV-----RFVLLANNLQIRGFKTKDEGTYRCGRILANGELINYDQIVAVVPTTQA 213
 OY 138 KPTVPQVRFKAVVGVGMATLHCQSESGHPRPHYSWRNDVPLPTDSRAPRRNSSHL 197
 DB 214 RQL-----RVANATNMAASVYLSC-DADGFPDPFELSWLKGEPI-EDGEKISF----- 260
 OY 198 NSETGLVFTVAFKEDPDGQYCYINSNDGSA 228
 DB 261 NEDSEMTIHVEKDDAEYSCTANNQAGEA 291
 RESULT 7
 ANAL DROME STANDARD; PRT; 333 AA.
 ID ANAL DROME
 AC PI5354; Q9V3A5;
 DT 01-APR-1980 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amalgam protein precursor.
 GN AMA OR BG:DS00276.6 OR CG2198.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RP
 RP STRAIN=Oregon-R.
 RC STRAIN=Oregon-R;
 RX MEDLINE=89028670; PubMed=3141062;
 RA Seeger M.A., Haffley L., Kaufman T.C.;
 RT "Characterization of amalgam: a member of the immunoglobulin
 superfamily from Drosophila."
 RL Cell 55:589-600(1988).
 RL [2]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Celniker S.E., Pfeiffer B.D., Kafets J., Martin C.H., Mayeda C.A.,
 RA Palazzolo M.J.;
 RT "Complete sequence of the Antennapedia complex of Drosophila."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter A.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baus A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Berns P.V., Berman B.P., Bhandari D., Boltsakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

DB 66 GDIRGLVCYNKIKTASYNENR-TFSDDTGTTTFSVTRKDTGMKTC-MVSDGEGNTYGEVTV 123

QY 132 ELTVQVKEPTVPCRYPKAVPVGKATLHCQESSEGHPRPHYSYWRNDVLPFTDSRANPRFR 191

DB 124 QILIVAPPEKPTINVPSSVTITGTRAVLTCSERDSSPPSSYKFKGVEMPLEPKSNRFS 183

QY 132 NSSSHINSETGLVFTAVHKDSSGQYTCIASND-AGSARCEQENEVTDLNIGIGVYL 250

DB 184 NSSYTLNOKTGLIFDPVASASDTGFTCOQNGYASPVKSDVPHNDVAVELNVGIVAAVF 243

QY 251 VVLAVALITLIGICCAVRRGYFINNKODESYKNGKPDGVYIRTD--EEGDFRHKSSF 308

DB 244 VTLILGLALIFETWFAISKGYTFDRAKK-GTSNKK-----VYSGPNARSDEFPQTSSF 296

QY 309 VT 310

DB 297 LV 298

RESULT 5

AC A33_HUMAN STANDARD; PRT; 319 AA.

AC Q99795; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cell surface A33 antigen precursor (Glycoprotein A33).

GN CPA33.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Colon carcinoma;

RA MEDLINE=97165045; PubMed=9012807;

RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J., Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C., Scott A.M., Rittler G., Cohen L., Welter S., Old L.J., Nice E.C., Burgess A.W.;

RA "The human A33 antigen is a transmembrane glycoprotein and a novel member of the immunoglobulin superfamily";

RT Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).

RL [12]

RP POST-TRANSLATIONAL MODIFICATIONS.

RA MEDLINE=97396159; PubMed=9245713;

RA Rittler G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W., Moritz R.L., Ji H., Heath J.K., White S.J., Welter S., Old L.J., Simpson R.J.;

RT "Characterization of posttranslational modifications of human A33 antigen, a novel palmitoylated surface glycoprotein of human gastrointestinal epithelium.";

RL Biochem. Biophys. Res. Commun. 236:682-686(1997).

CC -1- FUNCTION: May play a role in cell-cell recognition and signaling.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed in normal gastrointestinal epithelium and in 95% of colon cancers.

CC -1- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED CARBOHYDRATE.

CC -1- PTM: Palmitoylated.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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CC EMBL; U79725; AAC50957.1; -.

DR Genew; HGNC:4445; GPA33.

DR MIN; 602171; -.

DR GO; GO:0005888; C:plasma membrane integral to plasma membrane; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein; Transmembrane; Signal; Antigen.

KW SIGNAL

FT CHAIN 1 21 CELL SURFACE A33 ANTIGEN.

FT DOMAIN 22 319 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 22 235 POTENTIAL.

FT DOMAIN 235 256 POTENTIAL.

FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 22 134 IG-LIKE V-TYPE.

FT DOMAIN 140 227 IG-LIKE C2-TYPE.

FT DISULFID 258 261 POLY-CYS.

FT DISULFID 43 117 POTENTIAL.

FT DISULFID 146 222 POTENTIAL.

FT DISULFID 162 211 POTENTIAL.

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).

SC SEQUENCE 319 AA; 35632 MW; 9BFC7A4F45C2408E CRC64;

Query Match 14.28; Score 231.5; DB 1; Length 319;

Best Local Similarity 26.88; Pred. No. 3.7e-12; Indels 41; Gaps 13;

Matches 81; Conservative 46; Mismatches 134;

QY 29 IGAVNLKSSNRTPVPCRYPKAVPVGKATLHCQESSEGHPRPHYSYWRNDVLPFTDSRANPRFR 83

DB 19 VDAISVETPDVLRASGKSVTLPCYHTSTSSREGHICWDKLLNHTERVIWPFENKN 78

QY 84 -IQGDL-----AGREILIKTSIKRMVTRDSALYREYVARDKDEIDVIELTV 135

DB 79 YIHSEIKRNVSISSNNE-OSDASITTDQLTMADNGTEYCSVLSLSENTSRVRLV 137

QY 136 QVKEVTPVPCRYPKAVPVGKATLHCQESSEGHPRPHYSYWRNDVLPFTDSRANPRFR 195

DB 138 LVPSKRECGEGEGTILGNIGILQCSKESPTQGSWKRYNINLNGQPLAQASGQPV 197

QY 196 HLNSEGTGLVFTAVHKDSSGQYTCIASNDGASRCE-EQMEYVDNIG--GIGVYL 251

DB 198 LKNIST-----DTSGYVICTSSNEGTQFCNTTAVRSPNNVALYVIAVGVA 247

QY 252 VVLAVALITLIGICCAVRRGYFIN-NKQD-----ESYKNGKPDGVYI--RTDEGDFR 303

DB 248 ALIILIGIIVCCC--RGKMDMTEDKEDARPRAEVEE--PEQLRELSRESEEDDYR 302

QY 304 HK 305

DB 303 QE 304

RESULT 6

NCAL_XENLA STANDARD; PRT; 1088 AA.

AC P16170; 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180).

GN NCAM1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_Taxid=8355;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).

RA MEDLINE=90098871; PubMed=2481269;

```
CC -|- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AF11713; AAD42050.1; -
CC EMBL; AF207907; AAF22829.1; -
CC EMBL; AF172398; AAD48877.1; -
CC EMBL; AL136649; CAB66584.1; -
CC EMBL; AY358896; AAO89255.1; -
CC EMBL; BC001533; AAH01533.1; -
CC PIR; A59406; S56749; -
CC Genew; HGNC:14685; F11R.
CC MIM; 605721; -
CC GO; GO:0005911; C:intracellular junction; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR007110; IG-1like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00406; IgV_1.
CC PROSITE; PS00835; IG_LIKE_2.
CC TIGHT junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC FT SIGNAL; 1 25 POTENTIAL.
CC FT CHAIN; 26 299 JUNCTIONAL ADHESION MOLECULE 1.
CC FT DOMAIN; 26 238 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM; 239 259 POTENTIAL.
CC FT DOMAIN; 260 299 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN; 27 125 IG-LIKE V-TYPE 1.
CC FT DOMAIN; 135 228 IG-LIKE V-TYPE 2.
CC FT DISULFID; 50 109 POTENTIAL.
CC FT DISULFID; 153 212 POTENTIAL.
CC FT CARBOHYD; 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 299 AA; 32583 MW; D9SDE2PEA23D2851 CRC64;

Query Match 25.6%; Score 419; DB 1; Length 299;
Best Local Similarity 32.8%; Pred. No. 6e-26;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

QY 8 RLALCARLPPEFLLEFRGLIGAVNLKSNRPVQGESEVSLGCIITDSQSPRIM 67
DB 9 KKLCL-----FIALILCSIALGSVYVHSEPEVRIPENNPVKLCAY--SGFSSRYVM 62
QY 68 KKIODEQTYYVFDNKKIQGLAGRAELIGKTSIKTNVTRDSALYRCEVAVANDRKEID 127
DB 63 KFDQGDTRLVVCKNNKLTASYEDRVFL-PTGITFYSVTRDGTGTYTC-MVSEEGNSYG 120
QY 128 EYIELTVQKPTPVQKAVPVGKMATLHCOSEEGHPHYSMYRVDPLPDSRYAN 187
DB 121 EVYKRLVLPSPKPTVNLSSATTGNRAVLTSQDGSPPSEYTFPKGIVVPTNPKST 180
QY 188 PFRNSSSHUNSETGLVPTAVHKDDSGQYYCTASNDAGSARCEO-EMEYVDLNGIIT 246
DB 181 RARNSNSVYNPTTGLVDFPLASDTGEYSCEARNGYGPMTSNMVRVAVRNVGIV 240
QY 247 GGLVVLAVLALLTIGCCAYRGGYFINKQDSES-----YKNGKRDGVNVIITDEEGP 302
DB 241 AAVLVLTLLIGLVFGIWPAYSRGHFDRTKGTSSKKVITYSPS-----ARSEGEF 291
QY 303 RHKSSPVI 310
DB 292 KQTSFLV 299
```

```
AC Q9XT56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE JUNCTIONAL adhesion molecule 1 precursor (JAM).
GN FILR OR JAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9323940; Pubmed=10395639;
RA Ozaki H., Ishii K., Horrichi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
CC -|- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PAR3. The association of the PAR3-PAR3 complex may
CC prevent the interaction of PAR3 with JAM1, thereby preventing
CC tight junction assembly (By similarity). Plays a role in
CC regulating monocyte transmigration involved in integrity of
CC epithelial barrier. Involved in platelet activation.
CC -|- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
CC association between PAR3 and PAR3B probably disrupts this
CC interaction (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -|- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -|- SIMILARITY: Belongs to the immunoglobulin-like V-type domains.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AF11714; AAD42051.1; -
CC InterPro; IPR007110; IG-1like.
CC InterPro; IPR003598; IG_c2.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00406; IGC2_1.
CC PROSITE; PS00835; IG_LIKE_2.
CC TIGHT junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC FT SIGNAL; 1 24 POTENTIAL.
CC FT CHAIN; 25 298 JUNCTIONAL ADHESION MOLECULE 1.
CC FT DOMAIN; 25 237 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM; 238 258 POTENTIAL.
CC FT DOMAIN; 259 298 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN; 28 124 IG-LIKE V-TYPE 1.
CC FT DOMAIN; 134 227 IG-LIKE V-TYPE 2.
CC FT DISULFID; 49 108 POTENTIAL.
CC FT DISULFID; 152 211 POTENTIAL.
CC FT CARBOHYD; 184 184 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 298 AA; 32456 MW; 714FELC1714769A2 CRC64;

Query Match 24.7%; Score 403.5; DB 1; Length 298;
Best Local Similarity 33.8%; Pred. No. 1.2e-26;
Matches 102; Conservative 48; Mismatches 15; Indels 27; Gaps 10;

QY 21 LLLFRGLI-----GAVNLKSNRPVQ--EFSEVSLGCIITDSQSPRIEMKIQ 71
DB 12 LLLFTSMILCSIALGRGV-----QTYEYPVAVPENNPVKLSC--SYGQFSSPRVEMKFT 65
QY 72 DEQTYVFDNKKIQGLAGRAELIGKTSIKTNVTRDSALYRCEVAVANDRKEIDIVI 131
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DR GO: GO:000515; F:protein binding, IPT.
 DR InterPro: IPR007110; Ig-Like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PS00935; IG_Like; 2.
 DR TIGR: TIGR00001; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW TIGR: TIGR00001; Immunoglobulin domain; Glycoprotein; Transmembrane;
 Repeat; Signal; 3D-structure.
 FT CHAIN 1 26 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 27 300 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 259 POTENTIAL.
 FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 122 IG-LIKE V-TYPE 1.
 FT DOMAIN 134 230 IG-LIKE V-TYPE 2.
 FT DISULFID 49 108 POTENTIAL.
 FT DISULFID 152 212 POTENTIAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97EC CRC64;

Query Match 27.5%; Score 449.5; DB 1; Length 300;
 Best Local Similarity 35.2%; Pred. No. 1.7e-30;
 Matches 105; Conservative 56; Mismatches 122; Indels 15; Gaps 7;

20 LLLPFGCLIGAV-----NIKSSNRPVVOEFPSEVLSGIIITDSQTSDEPRIMKKIODEQ 74
 11 LLLPFGCLIGAV-----NIKSSNRPVVOEFPSEVLSGIIITDSQTSDEPRIMKKIODEQ 68
 75 TTYVFDNKKIQQDLAPRAELIGKTSIKIWNTRDSALYRCSEVANSRKEIDEIVIELT 134
 69 TALVCNNSQITAPYADRV--TFSSSGITFSSVTRKNGEYTC--NVSEEGQNGEVAISHLT 126
 135 VOYKPTPVGRCVAVPVGMATLHGOSEBGRPHYSRYNDVPLPT--DSBANRFRNS 193
 127 VLVPRKPTISVSSSTTIGRAVLTCSEHDSPSPSYSMFKGISMLTDPAKKTAFNMS 186
 194 SSHLNSSTGLVTAHVAKDSDGQYICIASNDAGS--RCEQSEVYDNLIGIIGVLV 252
 187 SFIDKSGLLIPDPPTAFDSGEYVCOAQNGYGTARSEAAHDAVELNVGIVAALVT 246
 253 LAYLALITIGICAVRGYRINKKODGSEYKNGKRDGNYIRTDGDPFRKKSSTV 310
 247 LILGLIFGVWFAVSRNGIFETTKG---TAPGKRVIVSQPSRSEGFKQTSSFLV 300

RESULT 3

JAM1_HUMAN

ID JAM1_HUMAN STANDARD; PRT; 299 AA.

AC 095624; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet FII receptor) (UNQ264/PRO301).

GN FII OR JAM1 OR JCAM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=9323940; PubMed=10395639;

RA Oaki H., Ishii K., Horiochi H., Arai H., Kawamoto T., Okawa K.,

RA Yamatsu A., Kita T.,

RT Combined treatment of TNF-alpha and IFN-gamma causes redistribution

RT of junctional adhesion molecule in human endothelial cells."

RL J. Immunol. 163:553-557 (1999).

RN SEQUENCE FROM N.A.

RA Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,

RA Kornacki E.,

RT Molecular cloning and sequencing of the cDNA of FII receptor, a

RT novel Ig superfamily member from human platelets."

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RA Naik U.P., Naik M.U., Deleon P., Spychala J.;

RT "Cloning and characterization of PAM-1, a novel platelet adhesion

RT molecule involved in platelet activation."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=21154917; PubMed=11230166;

RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesl S.,

RA Ansgar W., Boecker M., Bloeker H., Bauersachs S., Blum H.,

RA Lauber J., Duisterhoef A., Beyer A., Koehner K., Strack N.,

RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe C., Heubner D.,

RA Wandt R., Korn B., Klein M., Poustka A.;

RT "Towards a catalog of human genes and proteins: sequencing and

RT analysis of 500 novel complete protein coding human cDNAs."

RL Genome Res. 11:422-435 (2001).

RN SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heidens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Kobbie E., Sanchez C., Schoenfeld J.,

RA Seisagiri S., Simmons L., Singh J., Smith V., Stinson U., Vagts A.,

RA Vandlen R., Watanabe C., Wieda D., Woods K., Xie M.-H., Yamasaki D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RL bioinformatics assessment."

RL Genome Res. 13:2265-2270 (2003).

RN SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uesdin T.B., Toshitsugu S., Carninci P., Prange C.,

RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McGowan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.U., Huilyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Weare R.M.,

RA Butterfield Y.S.N., Krzywicki M.I., Skalska T., Smalins D.E.,

RA Scherch A., Schein J.E., Jones S.J.W., Metra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-1- FUNCTION: Seems to play a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PAR3. The association of the PAR3-PAR6 complex may prevent the interaction of PAR3 with JAM, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

-1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The association between PAR3 and PAR6B probably disrupts this interaction (By similarity).

-1- TISSUE SPECIFICITY: Type I membrane protein (potential). Epithelial and endothelial cells.

CC -1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENUES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- DATABASE: NAME=PROV; NOTE=PROV 2:1-3(2001).
CC WWW=http://www.ncbi.nlm.nih.gov/prov/guide/1652492186.g.htm".
CC -----
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CC EMBL; AF255910; AAF81223.1; -
CC EMBL; AF016009; AAG49022.1; -
CC EMBL; BC017779; AAH17779.1; -
CC Genew; HGNC:14686; JMW2.
CC MIM: 606870; -
CC DR GO: 0005887; C: integral to plasma membrane; NAS.
CC DR GO: 0016337; P: cell-cell adhesion; NAS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003598; IG_c2.
CC DR Pfam; PF00047; IG; 2.
CC DR SMART; SM00408; IGc2; 1.
CC DR PROSITE; PS00835; IG_LIKE; 2.
CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 298 POTENTIAL.
CC FT DOMAIN 21 238 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 239 259 POTENTIAL.
CC FT DOMAIN 260 298 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 32 127 IG-LIKE V-TYPE.
CC FT DOMAIN 134 128 IG-LIKE C2-TYPE.
CC FT DISULFID 50 109 POTENTIAL.
CC FT DISULFID 155 214 POTENTIAL.
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 298 AA; 33207 MW; CA78E518B22DCAEE CRC64;
Query March 29.5%; Score 483; DB 1; Length 298;
Best local similarity 36.2%; Pred. No. 2.5e-33;
Matches 115; Conservative 59; Mismatches 116; Indels 28; Gaps 10;
QY 1 MAIRRRPRLRLCARLPDFLLLRGCLIG----AVNLKSSNTPPVQ--EFSEVELSC 53
DB 1 MARSRHRL-----LILLRLYLVALGYKAYGAFSPKQOVVAVVEYGEALILAC 50
QY 54 IITDSQTSRPRLEMKKIODEQTYVFFNFKIQSLAGRAELTGSTLRKINNVRRDSALY 113
DB 51 -KTPKKTIVSRLEMKL--GRSVSFYVQQTLOQGFKNRAEMI-DFNIRIKNVRISDGKY 107
QY 114 RCEVAVNRDR-KEIDEIVIELTVQYKPTVPCRAVPKAVPVKATLHCQSESEGHPRPHYS 172
DB 108 RCEVAVPEEQGNLEEDVTLEVLVAPAVPSCVPSALSTGVLELRCQDEGNPAREYT 167
QY 173 WYRNDVPLPTDSRANPRFRNSSSHNSTGLVTAHKDSSGQYCIASNDASARCEE 232
DB 168 WPKDSIRLLENPRLOSQSTNSYTNMTKTGLQNTWYSKLDITGEVSCENRNVSVIRCPG 227
QY 233 QMEVYVDNLIGGIIGGVVLVALITLGIICAVRAGYFINNKDGESEYKPKPDGVN 292
DB 228 KRMGVDDNLINIGIIAAVVVVALVISVGLGVCAQRKGYF--SKE--TSFQ---KSNSSS 280
QY 293 YIRDSBEGDFRKKSFVI 310

DB 281 KATWSENDPHTKTSFII 298
RESULT 2
JMW1_MOUSE
ID JMW1_MOUSE STANDARD; PRT; 300 AA.
AC 086732;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN FILR OR JMW1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.,
RT "Functional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration.";
RT J. Cell Biol. 142:117-127(1998).
RN (2)
RP INTERACTION WITH PAR3.
RX MEDLINE=21340265; PubMed=11447115;
RA Ebner K., Suzuki A., Horikoshi Y., Hirose T.,
RA Meyer zu Bruckwede M.-K., Ohno S., Vestweber D.,
RT "The cell polarity protein Aip1/PAR-3 directly associates with
RT junctional adhesion molecule (JAM).";
RL EMO J. 20:3738-3746(2001).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX MEDLINE=21391702; PubMed=11500366;
RA Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA Schmid G., Mueller F., Bazzoni G., Dejana E., Bartal T.,
RA Winkler F.K., Hennig M.,
RT "X-ray structure of junctional adhesion molecule: structural basis for
RT homophilic adhesion via a novel dimerization motif.";
RL EMO J. 20:4391-4398(2001).
CC -1- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PAR3. The association of the PAR6-PAR3 complex may
CC prevent the interaction of PAR3 with JMW1, thereby preventing
CC tight junction assembly. Plays a role in regulating monocyte
CC transmigration involved in integrity of epithelial barrier.
CC Involved in platelet activation.
CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
CC association between PAR3 and PAR63 probably disrupts this
CC interaction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
CC cells.
CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC EMBL; U89915; AAC32982.1; -
CC PDB; 1F97; 22-AUG-01.
DR MGD; MGI:1321398; Filr.

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:08:53 ; Search time 17 Seconds
(without alignments)
949.515 Million cell updates/sec

Title: US-09-831-805a-6

Perfect score: 1635
Sequence: 1 MALRRPRLCAFLPPFL.....VNTIRDESGDFHKSFFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	29.5	298	JAM2_HUMAN	P57087 homo sapien
2	449.5	27.5	300	JAM1_MOUSE	O88792 mus musculu
3	419	25.6	299	JAM1_HUMAN	O95624 homo sapien
4	403.5	24.7	298	JAM1_BOVIN	O95624 bos taurus
5	233.5	14.2	319	A33_HUMAN	O95795 homo sapien
6	186	11.4	1088	NCAL_XENLA	P16170 xenopus lae
7	180	11.0	333	AVAIL_DROME	P15364 drosophila
8	177	10.8	1092	NCAL_XENLA	P26335 xenopus lae
9	171.5	10.5	725	NCAL_MOUSE	P13595 mus musculu
10	171.5	10.5	1115	NCAL_MOUSE	P13595 mus musculu
11	171	10.5	1377	NCAL_MOUSE	P13595 mus musculu
12	170.5	10.4	858	NCAL_RAT	P13596 rattus norv
13	169.5	10.4	1912	PRPD_HUMAN	P23468 homo sapien
14	165	10.1	837	NCAL_HUMAN	O15048 homo sapien
15	164.5	10.1	1051	PTK7_CHICK	O95793 mus musculu
16	164.5	10.1	3707	NCAL_MOUSE	O5136 mus musculu
17	164	10.0	837	NCAL_MOUSE	P13595 mus musculu
18	163.5	10.0	853	NCAL_BOVIN	P13595 mus musculu
19	163	10.0	1493	NCAL_MOUSE	P13595 mus musculu
20	162.5	9.9	6632	UNB9_CAEEL	O01761 caenorabdi
21	161.5	9.9	365	CXAR_HUMAN	P13550 homo sapien
22	158	8.7	1091	NCAL_CHICK	P13552 homo sapien
23	155.5	8.5	761	NCAL_HUMAN	P13552 homo sapien
24	155.5	8.5	848	NCAL_HUMAN	P13552 homo sapien
25	155.5	9.5	761	NCAL_HUMAN	P13552 homo sapien
26	153.5	9.4	1284	NCAL_CHICK	P13551 homo sapien
27	153	9.4	1461	NCAL_CHICK	P13551 homo sapien
28	151.5	9.3	349	NCAL_HUMAN	P13551 homo sapien
29	151	9.2	353	NCAL_HUMAN	P13551 homo sapien
30	150.5	9.2	702	CEPU_CHICK	O90773 gallus gall
31	149.5	9.1	1897	PRPD_HUMAN	P23468 homo sapien
32	149	9.1	338	LAMP_HUMAN	O62813 rattus norv
33	148.5	9.1	338	LAMP_RAT	O62813 rattus norv

34	148.5	9.1	646	1	MUL8_HUMAN	P43121 homo sapien
35	148	9.1	344	1	NTR1_MOUSE	O99910 mus musculu
36	147	9.0	344	1	NTR1_RAT	O62718 rattus norv
37	146.5	9.0	338	1	LAMP_HUMAN	O13449 homo sapien
38	146	8.9	365	1	CXAR_MOUSE	P97792 mus musculu
39	145.5	8.9	345	1	OPCM_RAT	P97792 mus musculu
40	145.5	8.9	4391	1	PGEM_HUMAN	P98160 rattus norv
41	145	8.9	521	1	CEA1_MOUSE	P20273 homo sapien
42	144	8.8	847	1	CD22_HUMAN	P20273 homo sapien
43	143.5	8.8	1277	1	CAML_FUGRU	O98902 fuigu rubrip
44	143.5	8.8	1443	1	NEO1_CHICK	O90610 gallus gall
45	141	8.6	345	1	OPCM_BOVIN	P13834 bos taurus

ALIGNMENTS

RESULT 1
JAM2_HUMAN STANDARD; PRT; 298 AA.
ID JAM2_HUMAN
AC P57087
DT 16-OCT-2001 (Ref. 40, Created)
DT 16-OCT-2001 (Ref. 40, Last sequence update)
DT 10-OCT-2003 (Ref. 42, Last annotation update)
DE Junctional adhesion molecule 2 precursor (Vascular endothelial
DE junction-associated molecule) (VE-JAM).
GN JAM2 OR VJAM OR C21ORF43.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP TISSUE=Vascular endothelial cells;
RC MEDLINE=20317114; PubMed=10779521;
RX Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.,
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells."
RL J. Biol. Chem. 275:19139-19145(2000).
[2]
RP TISSUE=Placenta;
RC MEDLINE=20507930; PubMed=10945976;
RX Cunningham S.A., Arrate M.P., Rodriguez J.M., Biercke R.J.,
RT "A novel protein with homology to the junctional adhesion molecule:
RT Characterization of leukocyte interactions."
RL J. Biol. Chem. 275:34750-34756(2000).
[3]
RP TISSUE=Lung;
RC MEDLINE=22386257; PubMed=12477932;
RX Klausner R.L., Petrigold E.A., Grouse L.H., Derge J.G.,
RT "Klauser R.L., Collins F.S., Wagner C.M., Schuler G.D.,
RT Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RT Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RT Diachenko L., Marutka K., Farmer A.A., Rubin G.M., Hong L.,
RT Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scherz T.E.,
RA Brownstein M.J., Ueda T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rada S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosk S.A., McKen P.U., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kelleman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smilins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Best Local Similarity 27.0%; Pred. No. 8.1e-05;
Matches 63; Conservative 35; Mismatches 74; Indels 61; Gaps 13;
Db 1 MALLRPPRLICARLPDFLLLRGCLIGAVLKSSNRTPVOEFSEVLSCTITDSQT 60
2428 LSVHPPPTVSV---LPE-----GPHVYKMG-----KDLTLCISSEPR 2463
QY 61 SDPRLEMKKIQDEQTYVFNKIQGLAGAEILGTSKIMVNRDALSARCVAR 120
Db 2464 SSPR-W-----TRIGTPVKLEPRKFGIMN--SHAMTKIASVKSXDGTVCQ--AQ 2509
QY 121 N---DRKEIDIEIVELTVQVPTVPCVPEKA---VPVGMATLHCQSESGHPRPHYSM 173
Db 2510 NALGTAQKQV-ELIYD-TGTVAPGTPQVQVESELTLEAGHTATLHC-SATGNPPTIHM 2566
QY 174 YRNDVPLPTBDRANPRFNSSSHLNSGTGLVPTAVAKDSDGOYVCYASNDAG 226
Db 2567 SKLRAPLPWQRI-----EGNTLVIPRVAQDSGQYICNATNSAG 2606

RESULT 14

neural cell adhesion molecule short domain form precursor - bovine

N.Alternate names: NCAM-140

C.Species: Bos primigenius taurus (cattle)

C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C.Accession: A32976; A38778; B44290; S05402

R.Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki

FEBS Lett. 254, 69-73, 1989

A.Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and

A.Reference number: A32976; MUID:89378239; PMID:2776887

A.Molecule type: mRNA

A.Residues: 1-853 <LIP>

A.Cross-References: GB:X16451; NID:960; PIDN:CAA34470.1; PID:G61

A.Accession: A38778

A.Molecule type: protein

A.Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;

A.Note: The authors identified this protein as calmodulin-independent adenylate cyclase

R.Rougon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A.Title: Structural and immunological characterization of the amino-terminal domain of m

A.Reference number: A44290; MUID:86140120; PMID:3512556

A.Accession: B44290

A.Molecule type: protein

A.Residues: 20-36 <RCU>

A.Note: 23-Glu was also found

C.Comment: Various forms of NCAM are produced by alternative splicing.

C.Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C.Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; su

F.1-19/Domain: signal sequence #status predicted <SIG>

F.20-853/Product: neural cell adhesion molecule, short domain form #status experimental

F.34-98/Domain: immunoglobulin homology <IMM1>

F.132-191/Domain: immunoglobulin homology <IMM2>

F.152-156/Region: heparin binding #status predicted

F.161-165/Region: heparin binding #status predicted

F.228-288/Domain: immunoglobulin homology <IMM3>

F.321-396/Domain: immunoglobulin homology <IMM4>

F.428-490/Domain: immunoglobulin homology <IMM5>

F.527-604/Domain: fibronectin type III repeat homology <FN3A>

F.633-693/Domain: fibronectin type III repeat homology <FN3B>

F.720-737/Domain: transmembrane #status predicted <TM>

F.738-853/Domain: intracellular #status predicted <INT>

F.11-96;139-189;235-286;328-394;435-488/Disulfide bonds: #status predicted

F.222;314;346;452;458;487/Binding site: carbohydrate (Asn (covalent) #status predicted

Query Match 10.0%; Score 163.5; DB 1; Length 853;

Best Local Similarity 27.3%; Pred. No. 1.7e-05;

Matches 63; Conservative 34; Mismatches 89; Indels 45; Gaps 11;

QY 27 CLIAA-----VNLKSNR-----TPVOEFSEVLSCTITDSQTS-DPRLEMKKIQ 71
Db 96 CVVAIEDGTESEATVNVKLFQKLMFQALPTPOFREGEDAVIVCDVSSLPITLIK-- 152
QY 72 DEQTYVFNKIQGLAGAEILGTSKIMVNRDALSARCVAR 129
Db 153 -----HKGRDVIILKQV--RFIVLTNNYLOIRGIKKTDEGTGRCGRILARG---EINRK 202
QY 130 VIELTVQVKEPTVPCR--VPKAVPGKMATLHCQSESGHPRPHYSYRNDVPLPTDSRAN 187
Db 203 DIQIVNVPPVOARQSIATVATNANLQDSVTLVC--NKEGFPEPFTVATKQGEQENDEDEK 261
QY 188 PRFNSSSHLNSGTGLVPTAVAKDSDGOYVCYASNDAGSARCEQEMEVY 238
Db 262 YLFSDDSSE-----LTIRKVDKNDAEYVCIAENKAG-----EQDASIH 300

RESULT 15

protein UNC-89 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999

C.Accession: T29757

R.Du, Z.; Le, T.T.; Wilson, R.

submitted to the EMBL Data Library, May 1997

A.Description: The sequence of C. elegans cosmid C09D1.

A.Reference number: 220679

A.Accession: T29757

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-6642 <DUZ>

A.Cross-References: EMBL:AF00331; PIDN:AA54132.1; GSPDB:GN00019; CESP:unc-89

A.Experimental source: strain Bristol N2; clone C09D1

A.Gene: CESP:unc-89

A.Map position: 1

A.Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/3; 352/3; 426/2; 454/1; 500/1; 537/1; 6

/; 5917/1; 6037/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match

Best Local Similarity 9.8%; Score 162.5; DB 2; Length 6642;

Matches 71; Conservative 39; Mismatches 93; Indels 125; Gaps 12;

QY 45 EFSEVELSCITDSQTS-----DPRLEMKK--IQDEQTYVFNKIQGLAGEA 92

Db 3828 EFVELLSCTVTERKQALCKKVGEPKIKWTKEGKEVMSARVRAEHKDGTL---- 3883

QY 93 EILGKTSKIMVNRDALSARCVAR-----VVAARDKEIDIEIVELTVQYK 138

Db 3884 -----ILTFNVTQALAGRCBAENYSSANTEGPIITLEGAKRIDGADFLQPKR 3937

QY 139 PVTVCVAPKAVPVGKMATLHCQSESGHPRPHYSYRNDVPLPTDSGRANPRFNSSSHN 198

Db 3988 PA-----VVTVGGEAVLEGKIS--GKPPSVYKNGEEL-----KPSDKVTENED 3982

QY 199 SETGLVFTAVAKDSDGOYVCYASNDAG-----SARCEQ 233

Db 3993 DGTQRLITVNAKDDMEYCEASNEFGDPSVDTLTVKPAQVAPGFPELSAIVKELT 4042

QY 234 EMEVYDNLIGGIIGGLVLAVALTLTGICCAVRRGVIINFKQGESYKNPKP----- 288

Db 4043 ETARFECKVSG-----TRPDVKWFD--GTPUKEDK 4071

QY 289 -----DGNVYI-----RTDEGDR 303

Db 4072 RVHPESTDDGQRLVIDSKTDGQGNR 4099

Search completed: April 12, 2004, 09:16:45

Job time : 22 secs

R;adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yada
Cancer Res. 52, 737-740, 1992
A>Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A/Reference number: A44929; MUID:92119637; PMID:1370651
A/Accession: B44929
A/Molecule type: mRNA
A/Residues: 1756-1804, 'C', 1806-1845 <ADA>
A/Cross-references: GB:S78086; NID:9243545; PIDN:AA21147.1; PID:9243546
A/Experimental source: pre-B cell NALM-6
A/Note: sequence extracted from NCBI backbone (NCBI:78086, NCBI:P:78087)
A/Note: the authors did not report the entire codon for residue 90
C/Genetics:
A/Gene: GDB:PTPRD
A/Cross-references: GDB:131384; OMIM:601598
A/Map position: 9p24-9p24
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
Oxy
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;38-100/Domain: immunoglobulin homology <IMM1>
F;140-209/Domain: immunoglobulin homology <IMM2>
F;250-304/Domain: immunoglobulin homology <IMM3>
F;711-811/Domain: fibronectin type III repeat homology <3FR>
F;1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1559/Binding site: substrate phosphate (Arg) #status predicted
F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 10.4%; Score 169.5; DB 2; Length 1912;
Best Local Similarity 28.6%; Pred. No. 1.4e-05;
Matches 65; Conservative 35; Mismatches 76; Indels 51; Gaps 13;

QY 39 RTPVVGFESVEVLSCTITDSQTPDR--IEM---KKIQDEQTYTFPDKKIQGLDAGSA 92
DB 28 RTFVDDQGVSGVASFQCA-TGDPFRKIVWNKKGVNSQREVELEFD-----GSG 79
OY 93 EIIQKTSIKITWNTVRPSALYRCGEVVARNDKEIDIEIVELTQVCPVTPVCRPKAVPV 152
DB 80 SVLRIGQLR---TPRDEAIYEC--VASNNVGEI-SVSTRILVLRAD-----QIPRGFPT 127
QY 153 GKX-----ATLHCQESBGRPHRYSYKRDVPLPTDSRANPFRNSSHLNE 200
DB 128 IDMGPOUKVERRTATMLCAAS-GNDPEITWFKFLPVDT-SNNNGRK---QLRSE 181
QY 201 T-----GTLVFTAVHKDSGGVYCIASNDAGSARCEQEMEYVDL 240
DB 182 SIGETPIRGALQIHQESSESQGRKECVATNSAGTRVAPANLVYREL 228

RESULT 12
A39712
Kinase-like protein klg precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C/Accession: A39712
R;Chou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A>Title: Characterization of a member of the immunoglobulin gene superfamily that possib
A/Reference number: A39712; MUID:91271300; PMID:1711213
A/Accession: A39712
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-1051 <CHO>
A/Cross-references: GB:M63437, NID:9212235; PIDN:AAA4893.1; PID:9212236
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C/Keywords: ATP
F;775-1046/Domain: protein kinase ATP-binding <KIN>
F;783-791/Region: protein kinase ATP-binding motif

Query Match 10.1%; Score 164.5; DB 2; Length 1051;
Best Local Similarity 24.5%; Pred. No. 1.8e-05;
Matches 66; Conservative 35; Mismatches 109; Indels 59; Gaps 11;

QY 40 TPVVOGFESVE-----LSCITITDSQTPDRLEWKKIQDEQTYTFPDKKIQGLDAGRAE 93
DB 486 TPPPOPLQCEWFEKNEKVTGSCATGRE--KPTIQWTLTD-----GSLPSBHSVRHG 534
QY 94 ILKRTSLKIMWNTVRPSALYRCGEVVARNDKEIDIEIVELTQVCPVTPVCRPKAVPV 153
DB 535 I-----LSFHKVSRSSGNVTC--IASNPQGGIRATVGLVAVYTFLEPEPTTVYQG 587
QY 154 KMATLHCQESBGRPHRYSYKRDVPLPTDSRANPFRNSSHLNEGTLYFTAVHKD 213
DB 588 HTAMFCCQ-AEGDPVPHIQWGRKIL-DPSKILPRIQIMPN-----GSLVYVDYTTBD 639
QY 214 SGQYVCIASNDAG-----SARCEGE-----MEYDINIGIIGVLY 251
DB 640 SGKTYCTAGNSCNIKREAFLYVVDKPALEDEGDSHPYKMTIQITGLSGVAAYVITII 639
QY 252 VLAVALITLIGICCAVARGYFINNKQDGE 280
DB 700 VLGLMF-----YCKKRRKAKRLKHPEGE 723

RESULT 13
S18252
heparan sulfate proteoglycan - mouse
N/Alternate names: perlecan
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
A/Accession: S18252; A31917, B31917, S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horisan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A>Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly
adhesion molecule.
A/Reference number: S18252; MUID:92078153; PMID:1744087
A/Accession: S18252
A/Molecule type: mRNA
A/Residues: 1-3707 <NO>
A/Cross-references: EMBL:M77174; NID:9200295; PIDN:AAA3991.1; PID:9200296
R;Noonan, D.M.; Horisan, E.A.; Ledbetter, S.R.; Vogel, G.; Sasaki, M.; Yamada, Y.; Haase
J. Biol. Chem. 263, 16379-16387, 1988
A>Title: Identification of cDNA clones encoding different domains of the basement membra
A/Reference number: A92680; MUID:89034110; PMID:2972708
A/Accession: A31917
A/Molecule type: mRNA
A/Residues: 940-1601 <NO2>
A/Cross-references: GB:J04054; NID:9200252; PIDN:AAA3989.1; PID:9200253
A/Accession: B31917
A/Molecule type: mRNA
A/Residues: 1870-2600 <NO3>
A/Cross-references: GB:J04055; NID:9200300; PIDN:AAA3992.1; PID:9200301
R;Schulze, B.; Mann, K.; Bartschutka, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A>Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A/Reference number: S66460; MUID:95377282; PMID:7649154
A/Accession: S66460
A/Molecule type: protein
A/Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C/Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe

C/Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1611-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;31670-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 164.5; DB 2; Length 3707;

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like fold
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F/1-15/Domain: signal sequence #status predicted <SIG>
F/20-1115/Product: neural cell adhesion molecule, long domain splice form #status expert
F/20-909,1077-1115/Product: neural cell adhesion molecule, short domain splice form #status expert
F/20-711/Domain: extracellular #status predicted <EXT>
F/24-98/Domain: immunoglobulin homology <IMM1>
F/132-191/Domain: immunoglobulin homology <IMM2>
F/152-156/Region: heparin binding #status predicted
F/161-165/Region: heparin binding #status predicted
F/228-290/Domain: immunoglobulin homology <IMM3>
F/262-272/Region: NCM binding #status predicted
F/323-388/Domain: immunoglobulin homology <IMM4>
F/420-482/Domain: immunoglobulin homology <IMM5>
F/519-596/Domain: fibronectin type III repeat homology <FN3A>
F/625-685/Domain: fibronectin type III repeat homology <FN3B>
F/712-729/Domain: transmembrane #status predicted <INT>
F/730-1115/Domain: intracellular #status predicted <INT>
F/91-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F/222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 171.5; DB 1; Length 1115;
Best Local Similarity 27.3%; Pred. No. 5.1e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

27 CLIGA-----VNLKSNR-----TPVOEFESVELSCITTDQTS-DPRLEKKIQ 71
96 CVTAEDGTQSEATVAVKIFQKLMFKNAPTPQEFKGEADVAVCVVSSLPETIIMK--- 152
Db
Qy 72 DEQTTVPFNKIQGLDLAGRAELIGKTLKIMVNRDLSALVRC--VVARNDKEIDEI 129
153 -----HKGRDVIILKKDV--RFYLSNNVYQIRGIKKTDEGTTCRGRIILARG--EINFK 202
Db
Qy 130 VIELTVQVFPVTPVCR--VPKAVPVGMATLHCQSEBGRPHRYMYRNDVPLPTDSRAN 187
203 DIQVIVNVPPTVQARQSIYVATNANLQGSVTLVC-DADGPEPTMTWTDGSEITENEE-D 260
Db
Qy 188 PRFRNSSHLNSETGLVFTAVHKDQSGYCYCIAISNDASACCEQEMEVY 238
261 EKSRSV---SDSEVTIRNVDKNDKDEAVYCIANKAG-----EQDASIH 302

RESULT 10

IDENTNC
neural cell adhesion molecule short domain form precursor - rat

N/Alternate names: NCM-140
C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 22-Jun-1999
C/Accession: S00846; B37795; I58136

R/Small, S.U.; Shull, G.B.; Santoni, M.J.; Akesson, R.
J. Cell Biol. 105, 2335-2345, 1987

A>Title: Identification of a cDNA clone that contains the complete coding sequence for a
A/Reference number: S00846; MUID:86059285; PMID:3680385

A/Molecule type: mRNA
A/Accession: S00846

A/Residues: 1-858 <SMA>
A/Cross-references: EMBL:X06564

R/Small, S.U.; Akesson, R.
J. Cell Biol. 111, 2089-2096, 1990

A>Title: Expression of the unique NCM VASE exon is independently regulated in distinct
A/Reference number: A37795; MUID:91035620; PMID:1699951

A/Accession: B37795
A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA
A/Residues: 340-81 <SM2>

R/Small, S.U.; Haines, S.L.; Akesson, R.A.
Neuron 1, 1007-1017, 1988

A>Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is de
A/Reference number: I58136; MUID:90166485; PMID:2483093

A/Accession: I58136
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 355-364 <RRS>

A/Residues: 355-364 <RRS>

A/Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C/Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mol
C/Comment: Various forms of NCM are produced by alternative splicing.
C/Genetics:

A/Genes: NCM

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like fold
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-858/Product: neural cell adhesion molecule, short domain form #status predicted <NA>
F/20-721/Domain: extracellular #status predicted <EXT>
F/34-98/Domain: immunoglobulin homology <IMM1>
F/132-191/Domain: immunoglobulin homology <IMM2>
F/152-156/Region: heparin binding #status predicted
F/161-165/Region: heparin binding #status predicted
F/228-290/Domain: immunoglobulin homology <IMM3>
F/262-272/Region: NCM binding #status predicted
F/323-388/Domain: immunoglobulin homology <IMM4>
F/430-492/Domain: immunoglobulin homology <IMM5>
F/529-606/Domain: fibronectin type III repeat homology <FN3A>
F/635-695/Domain: fibronectin type III repeat homology <FN3B>
F/722-729/Domain: transmembrane #status predicted <INT>
F/740-858/Domain: intracellular #status predicted <INT>
F/91-96,139-189,235-288,330-386,437-490/Disulfide bonds: #status predicted
F/222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 170.5; DB 1; Length 858;
Best Local Similarity 26.3%; Pred. No. 4.5e-06;
Matches 61; Conservative 41; Mismatches 85; Indels 45; Gaps 12;

27 CLIGA-----VNLKSNR-----TPVOEFESVELSCITTDQTS-DPRLEKKIQ 71
96 CVTAEDGTQSEATVAVKIFQKLMFKNAPTPQEFKGEADVAVCVVSSLPETIIMK--- 152
Db
Qy 72 DEQTTVPFNKIQGLDLAGRAELIGKTLKIMVNRDLSALVRC--VVARNDKEIDEI 129
153 -----HKGRDVIILKKDV--RFYLSNNVYQIRGIKKTDEGTTCRGRIILARG--EINFK 202
Db
Qy 130 VIELTVQVFPVTPVCR--VPKAVPVGMATLHCQSEBGRPHRYMYRNDVPLPTDSRAN 187
203 DIQVIVNVPPTVQARQSIYVATNANLQGSVTLVC-DADGPEPTMTWTDGSEITENEE--- 258
Db
Qy 188 PRFRNSSHLNSETGLVFTAVHKDQSGYCYCIAISNDASACCEQEMEVY 238
259 ---EDDEKHIFSDSSSLTIRNVDKNDKDEAVYCIANKAG-----EQDASIH 302

RESULT 11

A56178
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human

N/Alternate names: protein-tyrosine-phosphatase BPTP-2
C/Species: Homo sapiens (man)

C/Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text change 21-Jan-2000
C/Accession: A56178; S12052; B44929

R/Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Salto, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995

A>Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
A/Reference number: A56178; MUID:95204468; PMID:7696816

A/Accession: A56178
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-1912 <PUL>

A/Cross-references: GB:X38929; NID:g755652; PIDN:AA41749.1; PID:g755653
R/Krueger, N.X.; Streuli, M.; Salto, H.
EMBO J. 9, 3241-3252, 1990

A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase delta isoforms.
A/Reference number: S12049; MUID:91006018; PMID:2170109

A/Accession: S12052
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 390-1912 <KRU>

A/Cross-references: GB:X54133; NID:g935789; PIDN:CAA38068.1; PID:g935790
A/Note: The sequence from R13 SR is inconsistent with that from R17 SR having 568-T

Best Local Similarity 29.5%; Pred. No. 1.7e-06;
Matches 62; Conservative 26; Mismatches 86; Indels 34; Gaps 11

QY 30 GAVNLKSNR-----TPVQGEFSEVELSCITITDSQTDPR-IEWK-KIQDEQITVYFEDN 82
 Db 105 GYVNLKYQKLTETKAPLPQETFEGBDAVILICDVSSIPSIITWRHKGD-----VIFKK 159
 QY 83 KIQGDLGABEIIKETSILKINWYTRDSDALYRCE--TVARNDKEIDEIVIELTVQYKPV 140
 Db 160 DY-----RFLVLANNTLQIRGIKKTDEGNRCGRILARG---EINYKOIQIVANVPL 210
 QY 141 TPV--CRYPAVAVGKRNATLHQESEGHPRHYSWYANDVLPFDSDANPRFNSSHLN 198
 Db 211 IQARQIVRNATANNDESVLSC-DADGFPDPEISMLKGEPI-EDGEKISF-----N 261
 QY 199 SETGITVFLAHKDDSGQYCIASNDGSA 228
 Db 262 EDKSEMTTYRKEKEDAEYSCIANNQGEA 291

RESULT 8

neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse

C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000
C:Accession: A29673; S00382; A44290
R:Batchfile: D.; Santoni, M.V.; Wille, W.; Rupprecht, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A:Reference number: A29673; MUID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Residues: 1-725 <BAR>
A:Cross-references: EMBL:Y00051; NID:G53342; PID:CA66263.1; PID:G53343
R:Barbar, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-633, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM t

Query Match 10.5%, Score 171.5, DB 1, Length 725;

A:Molecule type DNA
 A:Residues: 642-656, 'D', 658-725 <BA2>
 A:Cross-references: EMBL:X07195
 R:Rougou, G.; Marshak, D.R.
 J. Biol. Chem. 261, 3396-3401, 1986
 A:Title: Structural and immunological characterization of the amino-terminal domain of n
 A:Reference number: A44290; MUID:86140120; PMID:3512556
 A:Accession: A44290
 A:Molecule type: protein
 A:Residues: 20-36 <ROU>
 C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
 C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:JUMG
 C:Genetics:
 A:Gene: NCAM
 A:Map position: 9
 A:Intons: 701/1
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:34-98/Domain: immunoglobulin homology <IMM1>
 F:133-191/Domain: immunoglobulin homology <IMM2>
 F:155-156/Region: heparin binding #status predicted
 F:161-165/Region: heparin binding #status predicted
 F:228-290/Domain: immunoglobulin homology <IMM3>
 F:268-272/Region: NCAM binding #status predicted
 F:323-368/Domain: immunoglobulin homology <IMM4>
 F:420-482/Domain: immunoglobulin homology <IMM5>
 F:519-596/Domain: fibronectin type III repeat homology <FN3A>
 F:628-665/Domain: fibronectin type III repeat homology <FN3B>
 F:41-96,139-189,235-288,330-386,427-480/Dissulfide bonds: #status predicted
 F:222,316,348,424,450,479/Binding site: carbohydrate (asn) (covalent) #status predicted

Best Local Similarity 27.3%; Pred. No. 3e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

QY 27 CILGA-----VULKSNR-----TPVOEFSVELSCITDQSNS-DRIMFKKIQ 71
||:||:||||:
Db 96 CVYTAEDG?QSEATYNVKI.FÖKLMEFNAPTEPBEFEGEDAVIVCVSSLEPTIIWK-- 152
QY 72 DEQTTFVFENDKIOGLAGRAELIGTSLKINWVRPSALYRCB--VVARDRKEIDEI 129
||:||:||||:
Db 153 -----HKGDVILKNV--RTVLSENNYLQINGIKKTBEGTTRCGGRLLARG--EIFK 202
QY 130 VIELTVQKPEVTIPVCR--VPKAPVPGKATLHCQESBGHPREPHYSWRNDVPLPTDSRAN 187
||:||:||||:
Db 203 DIOVINAVEPTVQARQISVNATANTANGQSVTLVC-DADGPFEFTMTXJDEGEIENEEE-D 260
QY 188 FFRNRSSSHINSETGLVFTAHHKDDSGGYCIASNDGSAACEOEHEMY 238
||:||:||||:
Db 261 ERRRSSV---SDSSEVTIRNVCKDEAYVIAENKKG---BQDSIH 302

RESULT 9

neural cell adhesion molecule 1 precursor, long domain splice form - mouse

N:Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C:Accession: A296773; S008473; S00384; A28281; A44290; S00383
R:Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaux, J.C.; Hirsch, M.R.; Fortacci,
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A:Reference number: A296773; MID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Reidites: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,'L',
A:Cross-references: EMBL:Y00051; NID:G53342; PID:N953343; CID:CA686263.1; PID:G53343
R:Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Gorlitz, C.; W.
Nucleic Acids Res. 15, 8621-8641, 1987
A:Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neurin

A:Accession: S00844
A:Molecule type: mRNA
A:Residues: 529-809,1077-1115 <S&N>
A:Cross-references: EMBL:X06328; NID:g55322; PIDN:CAA29641.1; PID:g817984
R:Barbae, J.A.; Chalk, J.C.; Steinhmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM tr
A:Reference number: S00382; MIMD:88243628; PMID:3396534
A:Accession: S00384
A:Molecule type: DNA
A:Residues: 642-1115 <BAR>
A:Cross-references: EMBL:X07195
R:Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A:Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse, s
A:Reference number: A28281; MIMD:88247757; PMID:2454455
A:Accession: A28281
A:Molecule type: mRNA
A:Residues: 804-1081 <BA3>
A:Cross-references: EMBL:X07244; NID:g55321; PIDN:CAA30230.1; PID:g929720
R:Rougou, G.; Marthak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A:Title: Structural and immunological characterization of the amino-terminal domain of m
A:Reference number: A44290; MIMD:86140120; PMID:3512556
A:Accession: A44290
A:Molecule type: protein
A:Residues: 20-36 <ROU>
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:JMSM
C:Genetics:
A:Gene: NCAM
A:Map position: 9
A:introns: 643/3; 701/1; 770/2; 809/2; 1076/2

F:1542/Binding site: substrate phosphate (Arg) #status predicted
F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 11.0%; Score 180.5; DB 2; Length 1894;
Best Local Similarity 28.8%; Pred. No. 1.7e-06;
Matches 72; Conservative 34; Mismatches 75; Indels 69; Gaps 15;

3 LRREPRRL-----CARLPDFLLLLFRGLIGAVNLKSNTPVQEFESVELSCIT 56
11 VRRRLSLTLFPLCACTPPRF-----TRTPVDQTVSGVASFLIC 52
57 DSGQSDPR--IEM---KRIODEQTVVFPDNKIQGLAGRAELIGKTSKINNVRRDS 110
53 QA-TGDRPKIVNNKKGVSNQRFVIEPDD-----GSGSVLRIGPLR---TPRDE 100
111 ALYCEVAVARNDKEIDEIVIELTVQVRYTPVGRVKAAPVGM-----ATL 158
101 ALYEC--VASNNVGEI--SVSTRLTIVLRD-----QIPRGEPITDMGQQLKVERTRTATM 152
159 HCOSEBGRPHRYGWRNDVPLPTDSRANPRFRSSSHLNSET--GLVFTAVAKHDSGOY 217
153 LCAAS-GNPDEITWFKDFLPVDI-SNNNGRIK---QLNSESIGALQIEQSESDQGX 206
218 YCIASNDAGS 227
207 ECVAATNSAGT 216

RESULT 5

A1923
amalgam protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C:Accession: A31923
C:Seeger, W.A.; Halfley, L.; Kaufman, T.C.
Cell 15, 589-600, 1988
A:Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D.
A:Reference number: A31923; PMID:89028670; PMID:3141062
A:Accession: A31923
A:Molecule type: DNA
A:Residues: 1-333 <SPR>
A:Cross-references: GB:M25561; NID:9156920; PIDN:AAA28367.1; PID:9156921
A:Gene: FlyBase:Ama
A:Genetics:
A:Cross-references: FlyBase:FBgn0000071

Query Match 11.0%; Score 180; DB 2; Length 333;
Best Local Similarity 26.8%; Pred. No. 2.3e-07;
Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;

35 KSNRPVQEFESVELSCITDSQSDPRIEWKIODEQTVVFPDNKIQGLAGRAEI 94
143 EMTPKSTLTVEGQNELTC--HANGFPKPTISMAR-----EHNAMVAGGHL 187
95 LGKTSKINNVRRDSALRCSEVARNRKEIDEIVIELTVQVRYTPVGRVKAAPVGM 154
188 LAEPTLRISVHMDRGYYC--IAQNGSGQDPKLRVFEVFRQIAVORPKIOMVSH 245
155 MATLHCOSEBGRPHRYGWRNDVPLPTDSRANPRFRSSSHLNSETGLVFTAVHKDS 214
246 SAELFC-SVQGYAPVAVVWKKNGVPL--OSSRHHEVANTASSSGTTSTVLRIDSGEDF 302
215 GQYTCIASNDAGA 228
303 GDYVCNATNKGHA 316

RESULT 6

JB0100
neural cell adhesion molecule 2 - African clawed frog
N:Alternate names: N-CAM 2
C:Species: Xenopus laevis (African clawed frog)

C:Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: JB0100
R:Kudo, M.; Takayama, E.; Tadokuma, T.; Shiohara, K.
Biochem. Biophys. Res. Commun. 245: 127-132, 1998
A:Title: Molecular cloning of 86d-form neural cell adhesion molecules (N-CAMs) as the ma
A:Reference number: JB0099; PMID:98204770; PMID:9535795
A:Accession: JB0100
A:Molecule type: mRNA
A:Residues: 1-725 <XUD>
A:Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BA25932.1; PID:g3116229
A:Experimental source: heart
A:Comment: This protein mediates and regulates various cell-cell interactions through bo
C:Superfamily: neural cell adhesion molecule, fibronectin type III repeat homology; immu
F:413-475/Domain: immunoglobulin homology <IMM>
F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.8%; Score 177; DB 2; Length 725;
Best Local Similarity 29.5%; Pred. No. 1.1e-06;
Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

30 GAVNLKSSNR-----TPVQEFESVELSCITDSQSDPR-IEMF-KIQDEQTVVFPDN 82
105 GTVNLKTVGKLFKXAPFQTEGEDAVIICDVASSIPSITVHKKGD-----VIFKX 159
83 KIQGLAGRAELIGKTSKINNVRRDSALYCE--VVARNDKREIDEIVIELTVQVRY 140
160 DV-----RFVLANNYQIRIKITDEGNVRCGRILRG--ELNKDIQVIVNVPPL 210
141 TPV--CRVKAAPVGVKATLHCOSEBGRPHRYGWRNDVPLPTDSRANPRFRSSSHLN 198
211 IQKQIRVAVATNMDSESVLSC-DADGPDPEISWLKKGEPI-EDGEKISF-----N 261
199 SETGTVFTAVAKHDSGOYTCIASNDAGA 228
262 EDKSEMTIYRKEKDEAEYSCIANNOAGEA 291

RESULT 7

UN0635
neural cell adhesion molecule 2 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C:Accession: UN0635
R:Jonsson, K.F.; Kriegl, P.A.
Gene 127, 243-247, 1993
A:Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are ex
A:Reference number: UN0635; PMID:93273239; PMID:7684721
A:Molecule type: mRNA
A:Accession: UN0635
A:Residues: 1-1092 <TON>
A:Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

A:Gene: NCM2
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
F:20-705/Domain: extracellular #status predicted <EXT>
F:324-95/Domain: immunoglobulin homology <IMM1>
F:129-188/Domain: immunoglobulin homology <IMM2>
F:149-153/Region: heparin binding #status predicted
F:158-162/Region: heparin binding #status predicted
F:317-381/Domain: immunoglobulin homology <IMM3>
F:413-475/Domain: immunoglobulin homology <IMM4>
F:512-589/Domain: fibronectin type III repeat homology <FN3A>
F:613-680/Domain: fibronectin type III repeat homology <FN3B>
F:706-723/Domain: transmembrane #status predicted <INT>
F:724-1092/Domain: intracellular #status predicted <INT>
F:41-93, 136-186, 232-282, 323-379, 420-473/Disulfide bonds: #status predicted
F:219, 310, 341, 417, 443, 472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

10.8%; Score 177; DB 1; Length 1092;

Db 241 AAVLVTLILGLIVFGIMFAVRSGHFDRTKKTSSKKVIVYSQPS-----ARSGEF 291

QY 303 RHKSPV 310

Db 292 KOTSSFLV 299

RESULT 2

JB0099

neural cell adhesion molecule 1 - African clawed frog

N/Alternate names: N-CAM 1

C/Species: Xenopus laevis (African clawed frog)

C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: J05009

R/Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohara, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A/Title: Molecular cloning of bsd-form neural cell adhesion molecules (N-CAMs) as the ma

A/Reference number: J05009; PMID:98204770; PMID:9535795

A/Accession: J05009

A/Molecule type: mRNA

A/Residues: 1-725 <KUD>

A/Cross-references: DDBJ:AB008162; NID:G3116226; PID:BA25931.1; PID:G3116227

A/Experimental source: heart

C/Comment: This protein mediates and regulates various cell-cell interactions through bc

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

F/413-475/Domain: immunoglobulin homology <IMM>

F/512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 11.4%; Score 187; DB 2; Length 725;

Best Local Similarity 29.9%; Pred. No. 1.6e-07;

Matches 63; Conservative 30; Mismatches 82; Indels 36; Gaps 12;

QY 30 GAVNLR-----SSNRTPVQEFSEVSLSCITDQTSQDR-LEWK-KIQDEQTVVFPDN 82

Db 105 GTVNLKIYOKLTFKNAPTQEFKEGEDAVIICDVSSISPIITWKKGD-----VIFRK 159

QY 83 KIQGLDAGAEILGKSLKIMWTRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137

Db 160 DV-----RFVLANNYLQIRGKIKTDEGTTCCEGRILARGINKDIQVIVNPPTIQ 213

QY 138 KPTVPQVRYKAVPVQKATLHCQSESGHPRPHYSWYRNDVLPDTSRANPRFNSSHL 197

Db 214 RQL-----RVNATKMAESVLSLSC-DADGFPDEISWLKKGEP-EDGEEKISF----- 260

QY 198 NSETGLVFTAHKDKDSQGYCIASNDAGSA 228

Db 261 NEDQSEMTIHVEKDEDAEYSCIANNQAGEA 291

RESULT 3

IOXNLT

neural cell adhesion molecule long domain form precursor - African clawed frog

N/Alternate names: NCM-180

N/Contains: neural cell adhesion molecule, short domain form (NCM-140)

C/Species: Xenopus laevis (African clawed frog)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C/Accession: S09600

R/Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.

Nucleic Acids Res. 17, 10321-10335, 1989

A/Title: Primary structure and developmental expression of a large cytoplasmic domain fo

A/Reference number: S09600; PMID:90058871; PMID:2481269

A/Accession: S09600

A/Molecule type: mRNA

A/Residues: 1-1088 <KRI>

A/Cross-references: EMBL:M55696; NID:G214609; PID:AAA49909.1; PID:G214610

A/Note: the authors translated the codon AAA for residue 970 as Ieu

C/Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mol

C/Comment: Several forms of NCM are produced by alternative splicing.

C/Genetics:

A/Gene: NCM

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LDI

F/20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pred

F/20-705/Domain: extracellular #status predicted <EXT>

F/34-95/Domain: immunoglobulin homology <IMM1>

F/129-188/Domain: immunoglobulin homology <IMM2>

F/149-153/Region: heparin binding #status predicted

F/158-162/Region: heparin binding #status predicted

F/225-284/Domain: immunoglobulin homology <IMM3>

F/317-381/Domain: immunoglobulin homology <IMM4>

F/413-475/Domain: immunoglobulin homology <IMM5>

F/512-589/Domain: fibronectin type III repeat homology <IMM6>

F/618-679/Domain: fibronectin type III repeat homology <IMM7>

F/706-723/Domain: transmembrane #status predicted <TM>

F/724-1088/Domain: intracellular #status predicted <INT>

F/41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted

F/219,310,341,417,443,472/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 11.4%; Score 186; DB 1; Length 1088;

Best Local Similarity 29.9%; Pred. No. 3.1e-07;

Matches 63; Conservative 30; Mismatches 82; Indels 36; Gaps 12;

QY 30 GAVNLR-----SSNRTPVQEFSEVSLSCITDQTSQDR-LEWK-KIQDEQTVVFPDN 82

Db 105 GTVNLKIYOKLTFKNAPTQEFKEGEDAVIICDVSSISPIITWKKGD-----VIFRK 159

QY 83 KIQGLDAGAEILGKSLKIMWTRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137

Db 160 DV-----RFVLANNYLQIRGKIKTDEGTTCCEGRILARGINKDIQVIVNPPTIQ 213

QY 138 KPTVPQVRYKAVPVQKATLHCQSESGHPRPHYSWYRNDVLPDTSRANPRFNSSHL 197

Db 214 RQL-----RVNATKMAESVLSLSC-DADGFPDEISWLKKGEP-EDGEEKISF----- 260

QY 198 NSETGLVFTAHKDKDSQGYCIASNDAGSA 228

Db 261 NEDQSEMTIHVEKDEDAEYSCIANNQAGEA 291

RESULT 4

C54689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor

N/Alternate names: NPTP delta type B/C

N/Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C/Species: Mus musculus (house mouse)

C/Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999

C/Accession: C54689; B54689

R/Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Mol. Cell. Biol. 13, 5513-5523, 1993

A/Title: NPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized

A/Reference number: A54689; PMID:93360986; PMID:8355657

A/Accession: C54689

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1894 <MI2>

A/Experimental source: brain; splice form B

A/Note: sequence inconsistent with nucleotide translation

A/Note: sequence extracted from NCBI database (NCBIN:137486, NCBIPI:137487)

A/Accession: B54689

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>

A/Experimental source: brain; splice form C

A/Note: sequence inconsistent with nucleotide translation

A/Note: sequence extracted from NCBI database (NCBIN:136530)

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i

C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F/45-107/Domain: immunoglobulin homology <IMM1>

F/245-299/Domain: immunoglobulin homology <IMM2>

F/317-399/Domain: fibronectin type III repeat homology <FNA3A>

F/1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F/1652-1874/Domain: protein-tyrosine-phosphatase homology <PMP2>

F/1536/Active site: Cys (phosphocysteine intermediate) #status predicted

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: April 12, 2004, 09:12:38 ; Search time 20 Seconds
(without alignments)
1490.969 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALTREPRLICARLPDFLL.....VNTIRDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419	25.6	299	S56749	junctional adhesio
2	187	11.4	725	JEO099	neural cell adhesi
3	186	11.4	1088	IJXN1L	neural cell adhesi
4	180.5	11.0	1894	C54689	protein-tyrosine-p
5	180	11.0	333	A31923	amalgam protein pr
6	177	10.8	725	JEO100	neural cell adhesi
7	177	10.8	1092	JUN035	neural cell adhesi
8	171.5	10.5	725	IJMSNG	neural cell adhesi
9	171.5	10.5	1115	IJMSNG	neural cell adhesi
10	170.5	10.4	858	IJRTNC	neural cell adhesi
11	169.5	10.4	1932	A56178	protein-tyrosine-p
12	164.5	10.1	1051	A39712	kinase-like protei
13	164.5	10.1	3707	S18252	heparan sulfate pr
14	163.5	10.0	853	IJB0NC	neural cell adhesi
15	162.5	9.9	6642	T29757	protein UNC-69 - C
16	161.5	9.9	1612	T30805	ducal protein - mo
17	161	9.8	7962	I38346	elastic titin - hu
18	159.5	9.8	1033	S19247	cell adhesion prot
19	158	9.7	3538	UC2457	vascular cell adhe
20	159	9.7	1333	PN0568	connexin 3B, chi
21	159	9.7	14162	T42633	connexin/citric -
22	157	9.6	1907	S50693	protein-tyrosine-p
23	156	9.5	1091	IJCHNL	neural cell adhesi
24	156	9.5	1501	I58148	protein-tyrosine-p
25	156	9.5	1863	S46217	protein-tyrosine-p
26	155.5	9.5	761	IJHNG	neural cell adhesi
27	155.5	9.5	1239	A43425	Bravo/Nr-CAM cell
28	155.5	9.5	1268	A39640	neural cell adhesi
29	154.5	9.4	495	T25750	hypothetical prote

30	153.5	9.4	365	2	JC7780	coxackie- and ade
31	153	9.4	352	2	T33433	hypothetical prote
32	153	9.4	875	2	T33434	hypothetical prote
33	152	9.3	483	2	T17346	hypothetical prote
34	151	9.2	1651	2	T14160	transmembrane rece
35	150.5	9.2	702	2	A36319	carcinoembryonic a
36	150	9.2	1262	1	B48758	protein-tyrosine-p
37	150	9.2	1496	1	A48758	protein-tyrosine-p
38	149.5	9.1	1897	1	TDHULK	leukocyte antigen-
39	149	9.1	521	2	S34338	leukocyte antigen-
40	149	9.1	1898	2	S46216	leukocyte antigen-
41	148.5	9.1	646	2	I38049	cell surface glyco
42	147.5	9.0	871	1	I48696	protein-tyrosine k
43	147.5	9.0	881	1	I48697	protein-tyrosine k
44	147	9.0	338	2	JCS519	50K glycoprotein p
45	147	9.0	344	2	I56551	neurotrophin - rat

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N:Alternate names: FII platelet antigen; platelet adhesion molecule PM-1; platelet FII
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: A59406; #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
R:Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
U. Immunol. 163, 553-557, 1999
A:Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A:Reference number: A59406; PMID:9323940; PMID:10395639
A:Accession: A59406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <O2A>
A:Cross-references: GB:AA02050; NID:G5326797; PIRN:AA02050.1
R:Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A:Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A:Reference number: S56749; PMID:9374438; PMID:7646439
A:Accession: S56749
A:Molecule type: protein
A:Residues: 28-45; 'X', 51-53; 62-73, 'E', 75-103; 123, 'F', 125-130; 'PDKDTIYANXY'; 'LT', 206, 'X'
A>Note: the order of the peptides other than the amino terminus was not determined
C:Gene: JAM
C:Genetics:
C:Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-299/Product: junctional adhesion molecule #status predicted <VAT>
Query Match 25.6%; Score 419; DB 2; Length 299;
Best local similarity 32.8%; Pred. No. 3.1e-27;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;
QY 8 RLRLCARLPDFLLFRGLIGAVNKSNNRTPVQEFSEVSLCITTDSPRIEW 67
DB 9 RKLILCT---FILAILCSIALGSLVYHSEPEPRRIENNPPVLTSCAY--SGFSSPVEW 62
QY 68 KKTIDDEQTYVFFEDNKIOGLAGRAELIGKTSIKMNVTRRDSALRCEVVAARDKEID 127
DB 63 KFDQGDTRLVAVCNKRTITASVEDRVPFL-PTGTFKSVTRBEDIGTYTC-MVSEBGGNSYG 120
QY 128 EIVIELTVQVKVTPVPCRVKAVGVGKATLHCOESGHRPHYSWYRNPVPLPTDSRAN 187
DB 121 EVKVLIVLPSPKPTVNIIESATIGRAVUTSGEQSGSPSEETWKKDGIWFTNKST 180
QY 188 PRFNSSSHLNSSETGLVFTVAHVKDSGGQYCIASNDAGARCEQ--EMEYDIANGIIT 246
DB 181 RAFNSSTVILNPPTGGVLFVPLSLASDTSGEVSCERNGYGTPTMSNAVRMAVENNVIV 240
QY 247 GGVTVLAVLALITLIGICARRGYFIINNODGSS---YKPNPKPGVNVYIRFDEGDF 302

PR 30-MAR-2000; 2000MO-US008439.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 25-MAY-2001; 2001US-0086034.
 XX
 XX (GENTH) GENENTECH INC.
 XX Botstein D, Desnovers L, Ferrara N, Fong S, Gao W, Goddard A,
 PI Gurley AL, Pan U, Roy MA, Stewart TA, Tumas D, Watanabe CK,
 PI Wood WI;
 DR WPI; 2002-665999/71.
 DR N-PSDB; ABS67460.
 PT New human secreted and transmembrane (PRO) polypeptides, useful for
 PT treating conditions requiring PRO polypeptides, for screening PRO
 PT antagonists and agonists useful as drug candidates.
 XX
 PS Claim 12; Fig 14; 125pp; English.
 XX
 CC The invention relates to new human secreted and transmembrane proteins
 CC (PRO) and nucleic acids of the invention. The polypeptides can be
 CC administered therapeutically, especially by expressing encoding
 CC polynucleotides, e.g. in therapeutic compositions. They can be used to
 CC screen for PRO polypeptide antagonists and agonists useful to identify
 CC drug candidates. They can also be used to produce antibodies, useful to
 CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
 CC therapeutically (e.g. as antagonists or to target and/or deliver
 CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
 CC produce antisense sequences to inhibit polypeptide production. They can
 CC be used to produce probes and primers useful to detect or isolate
 CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
 CC sequences from other species. They are also useful for gene mapping and
 CC to generate transgenic animals. ABS9135-ABS91363 represent human PRO
 CC amino acid sequences of the invention
 XX
 XX Sequence 310 AA;
 SQ
 Query Match 99.6%; Score 1629; DB 5; Length 310;
 Best Local Similarity 99.7%; Pred. No. 8.6e-131;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MALRRPRLRLCARLPDFLLFRGCLLIGAVNLKSNRTPVYCFESESVELSCITTDGQ 60
 DB 1 MALRRPRLRLCARLPDFLLFRGCLLIGAVNLKSNRTPVYCFESESVELSCITTDGQ 60
 QY 61 SPPRIEMKKIOBQOTTYVFPDNKIQDLAGRAELIGKTSIKMTNTRDSALYRCVVAR 120
 DB 61 SPPRIEMKKIOBQOTTYVFPDNKIQDLAGRAELIGKTSIKMTNTRDSALYRCVVAR 120
 QY 121 NDRKEIDELVIELTYOVKQVTPVCRPKAVPYGKATLHCOSEGHPRPHSWYNDVPL 180
 DB 121 NDRKEIDELVIELTYOVKQVTPVCRPKAVPYGKATLHCOSEGHPRPHSWYNDVPL 180
 QY 181 PTDSRANPFRNSSFHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSH 240
 DB 181 PTDSRANPFRNSSFHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSHLSH 240
 QY 241 NIGGIIGVLYVLAVALITTLGICCAVRRGYFINNKKOGESYONGKRGDGVVYRTDEG 300
 DB 241 NIGGIIGVLYVLAVALITTLGICCAVRRGYFINNKKOGESYONGKRGDGVVYRTDEG 300
 QY 301 DFRHKSSEVI 310
 DB 301 DFRHKSSEVI 310
 AC ABB84947;
 XX
 XX ABB84947 standard; protein; 310 AA.
 XX

XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1868 protein sequence SEQ ID NO:262.
 XX
 XX Human; angiogenesis; cardiast; cytoskeletal; antiangiogenic; hypotensive;
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 OS
 XX Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001MO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 02-AUG-2000; 2000US-0222655P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000MO-US023322.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-0064610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-MAR-2001; 2001MO-US006666.
 PR 09-MAR-2001; 2001US-00803706.
 PR 14-MAR-2001; 2001US-00806689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866026.
 PR 25-MAY-2001; 2001US-00865034.
 PR 25-MAY-2001; 2001MO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PU, Gurley AL, Halian KO, Marsters SA, Pan U,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88202.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 262; 565pp; English.
 XX

KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
 KW autoimmune hemolytic anaemia; diabetes mellitus; infectious hepatitis;
 KW psoriasis; allergic diseases of the lung; graft-versus host disease;
 KW tumour; gene therapy.
 XX Homo sapiens.
 OS US2002098506-A1.
 PV 25-JUL-2002.
 PF 27-DEC-2001; 2001US-00033301.
 XX 04-AUG-1998; 98US-0095325P.
 PR 16-DEC-1998; 98US-0112851P.
 PR 16-DEC-1998; 98US-0113145P.
 PR 22-DEC-1998; 98US-0113511P.
 PR 12-JAN-1999; 99US-0115558P.
 PR 12-JAN-1999; 99US-0115565P.
 PR 12-JAN-1999; 99US-0115733P.
 PR 09-FEB-1999; 99US-0119341P.
 PR 10-FEB-1999; 99US-0119537P.
 PR 12-FEB-1999; 99US-0119965P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 29-OCT-1999; 99US-0162506P.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 25-MAY-2001; 2001US-00866034.
 XX (GETH) GENENTECH INC.
 PA Boretstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CX,
 PI Wood WJ;
 WI: 2002-690475/74.
 DR N-PSDB; ABS68392.
 DR Novel secreted and transmembrane polypeptides and polynucleotides useful
 PT for diagnosis and treatment of inflammatory disorders and immune-related
 PT diseases, and identifying modulators.
 PS Claim 12, Fig 14; 125pp; English.
 XX The invention relates to an isolated polypeptide having at least 80%
 CC amino acid sequence identity to secreted and transmembrane polypeptides
 CC PRO1800, PRO359, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3334 or
 CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
 CC cells and antibodies against PRO polypeptides. PRO proteins are useful
 CC for identifying modulators of the polypeptide. PRO1868 useful for the
 CC diagnosis and treatment of inflammatory and immune related diseases
 CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
 CC sclerosis, autoimmune hemolytic anaemia, thyroiditis, diabetes mellitus,
 CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
 CC versus host disease and tumours. PRO nucleic acids are useful for
 CC constructing hybridisation probes for mapping the gene that encodes that
 CC PRO and for the genetic analysis of individuals with genetic disorders,
 CC and for generating transgenic animals which are useful in the development
 CC also useful for gene therapy, chromosome identification, and tissue
 CC typing. PRO proteins are useful as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies are useful in
 CC diagnostic assays for PRO, e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO. The present

CC sequence represents a PRO protein
 XX SQ Sequence 310 AA;
 Query Match 99.6%; Score 1629; DB 5; Length 310;
 Best Local Similarity 99.7%; Pred. No. 8.6e-131;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MALRRPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVYQFESVEVLSCTITDSQT 60
 DB 1 MALRRPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVYQFESVEVLSCTITDSQT 60
 QY 61 SDPRIEMKKIODEQTTTYVFPDKRIGDLAGRAELIGKTSLKIMNTRRDSALYRCEVVAR 120
 DB 61 SDPRIEMKKIODEQTTTYVFPDKRIGDLAGRAELIGKTSLKIMNTRRDSALYRCEVVAR 120
 QY 121 NDRKEIDEIVIELTVQKFPVPCVPAVYVGNKATTHCOESEGHPRPHYSWYNDVPL 180
 DB 121 NDRKEIDEIVIELTVQKFPVPCVPAVYVGNKATTHCOESEGHPRPHYSWYNDVPL 180
 QY 181 PTDSRANPRFRSSSHNSHSETGLVFTAVHKDSDGQYCIASNDAGSARCEQMEVYDL 240
 DB 181 PTDSRANPRFRSSSHNSHSETGLVFTAVHKDSDGQYCIASNDAGSARCEQMEVYDL 240
 QY 241 NIGGIIGVLYVLAVALITLIGICCAVRRGYFINNKODSESYKNFGKPDGVNVIPTDEEG 300
 DB 241 NIGGIIGVLYVLAVALITLIGICCAVRRGYFINNKODSESYKNFGKPDGVNVIPTDEEG 300
 QY 301 DFRHKSSFVI 310
 DB 301 DFRHKSSFVI 310
 RESULT 13
 ABG91361
 ID ABG91361 standard; protein; 310 AA.
 XX AC ABG91361;
 XX DT 29-NOV-2002 (first entry)
 XX XX Novel human secreted protein #7.
 DE Human; secreted protein; transmembrane protein; gene mapping; transgenic;
 KW immunogenic.
 XX Homo sapiens.
 OS US2002098505-A1.
 PV 25-JUL-2002.
 PF 28-DEC-2001; 2001US-00033246.
 XX 04-AUG-1998; 98US-0095325P.
 PR 16-DEC-1998; 98US-0112851P.
 PR 16-DEC-1998; 98US-0113145P.
 PR 22-DEC-1998; 98US-0113511P.
 PR 12-JAN-1999; 99US-0115558P.
 PR 12-JAN-1999; 99US-0115565P.
 PR 12-JAN-1999; 99US-0115733P.
 PR 09-FEB-1999; 99US-0119341P.
 PR 10-FEB-1999; 99US-0119537P.
 PR 12-FEB-1999; 99US-0119965P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.

23-JUL-1999; 99US-0145220P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA,
 Shi Y, Lafleur DM, Olsen HS, Birse CE, Komatsu GA;
 WPI; 2001-123261/13.
 New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
 preventing and treating e.g. autoimmune, hyperproliferative,
 cardiovascular, and ocular diseases or disorders and microorganism
 infections.
 Claim 11; Page 557-558; 601pp; English.
 The present invention relates to 29 human secreted proteins. The
 invention is used to prevent autoimmune diseases e.g. rheumatoid
 arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 disorders e.g. cerebral ischemia, angiodenesis, nervous system disorders
 e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 fungi and ocular disorders e.g. corneal infection. Also used in food
 preparations
 Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
 Best Local Similarity 99.7%; Pred. No. 8.6e-131;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSNRTPVQEFSEVELSCIITDSQT 60
 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSNRTPVQEFSEVELSCIITDSQT 60
 61 SDRPRLEMKIODEQTTVPFNDKIQGLAGRAELIGKTSLKIMNTRSDALYRCVVAR 120
 61 SDRPRLEMKIODEQTTVPFNDKIQGLAGRAELIGKTSLKIMNTRSDALYRCVVAR 120
 121 NDRKEIDEIVIELTVQVKPVPYCRVPAVPVGMATLHCQESGHPRHYSWYRNDVPL 180
 121 NDRKEIDEIVIELTVQVKPVPYCRVPAVPVGMATLHCQESGHPRHYSWYRNDVPL 180
 181 PDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCIASNDASARCEOEVEYDL 240
 181 PDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCIASNDASARCEOEVEYDL 240
 241 NIGGIIGVAVLAVALITLIGICCAVRGYPINNKGDESYKNGPKDPGVNIRITDEEG 300
 241 NIGGIIGVAVLAVALITLIGICCAVRGYPINNKGDESYKNGPKDPGVNIRITDEEG 300
 301 DFRHKSFEVI 310
 301 DFRHKSFEVI 310

RESULT 11
 AAB80409
 ID AAB80409 standard; protein; 310 AA.
 XX
 AC AAB80409;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Secreted protein encoded by gene #39.
 XX
 KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
 XX cerebrovascular; infection; food.
 XX
 OS Homo sapiens.
 XX
 PN MO200107459-A1.
 XX

01-FEB-2001.
 20-JUL-2000; 2000MO-US019735.
 23-JUL-1999; 99US-0145220P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA,
 Shi Y, Lafleur DM, Olsen HS, Birse CE, Komatsu GA;
 WPI; 2001-123261/13.
 New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
 preventing and treating e.g. autoimmune, hyperproliferative,
 cardiovascular, and ocular diseases or disorders and microorganism
 infections.
 Claim 11; Page 559-560; 601pp; English.
 The present invention relates to 29 human secreted proteins. The
 invention is used to prevent autoimmune diseases e.g. rheumatoid
 arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 disorders e.g. cerebral ischemia, angiodenesis, nervous system disorders
 e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 fungi and ocular disorders e.g. corneal infection. Also used in food
 preparations
 Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
 Best Local Similarity 99.7%; Pred. No. 8.6e-131;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSNRTPVQEFSEVELSCIITDSQT 60
 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSNRTPVQEFSEVELSCIITDSQT 60
 61 SDRPRLEMKIODEQTTVPFNDKIQGLAGRAELIGKTSLKIMNTRSDALYRCVVAR 120
 61 SDRPRLEMKIODEQTTVPFNDKIQGLAGRAELIGKTSLKIMNTRSDALYRCVVAR 120
 121 NDRKEIDEIVIELTVQVKPVPYCRVPAVPVGMATLHCQESGHPRHYSWYRNDVPL 180
 121 NDRKEIDEIVIELTVQVKPVPYCRVPAVPVGMATLHCQESGHPRHYSWYRNDVPL 180
 181 PDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCIASNDASARCEOEVEYDL 240
 181 PDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCIASNDASARCEOEVEYDL 240
 241 NIGGIIGVAVLAVALITLIGICCAVRGYPINNKGDESYKNGPKDPGVNIRITDEEG 300
 241 NIGGIIGVAVLAVALITLIGICCAVRGYPINNKGDESYKNGPKDPGVNIRITDEEG 300
 301 DFRHKSFEVI 310
 301 DFRHKSFEVI 310

RESULT 12
 ABG92709
 ID ABG92709 standard; protein; 310 AA.
 XX
 AC ABG92709;
 XX
 DT 18-NOV-2002 (first entry)
 XX
 DE Human secreted protein PRO1868.
 XX
 KW Human, secreted and transmembrane protein; PRO1860; PRO539; PRO962;
 XX PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
 XX inflammatory disorder; immune related disease; rheumatoid arthritis;

polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFESVELSCIITDSOT 60
DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFESVELSCIITDSOT 60
QY 61 SDRPIEMKKIOBQTYVFFDNKIOGDLGRAEILIGKSLKIMNTVRDSALYRCEVVAR 120
DB 61 SDRPIEMKKIOBQTYVFFDNKIOGDLGRAEILIGKSLKIMNTVRDSALYRCEVVAR 120
QY 121 NDRKEIDELIVELTVQVKVPTVPCRVKPAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDELIVELTVQVKVPTVPCRVKPAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLSEGTGLVFTAVHKDQSGQYCIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSSHLSEGTGLVFTAVHKDQSGQYCIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGVLLVLAVALITLIGICAYRRGYFINNKODGESYKPKPGVNYIRTBEG 300
DB 241 NIGGIIGVLLVLAVALITLIGICAYRRGYFINNKODGESYKPKPGVNYIRTBEG 300
QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

RESULT 9

AAB80383
ID AAB80383 standard; protein; 310 AA.

AC AAB80383;

DT 24-APR-2001 (first entry)

DE Secreted protein encoded by gene #13.

KM Secreted protein; human; autoimmunity; hyperproliferation; cardiovascular;

KW cerebrovascular; infection; food.

OS Homo sapiens.

PN WO200107459-A1.

PD 01-FEB-2001.

PF 20-JUL-2000; 2000WO-US019735.

PR 23-JUL-1999; 99US-0145220P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM, Edner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Latteur DW, Olsen HS, Birse CE, Komatsu CA;
DR WPI; 2001-123261/13.

XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmunity, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.

PS Claim 11; Page 538-539; 601pp; English.

CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations

Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFESVELSCIITDSOT 60
DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSNRTPVVOEFESVELSCIITDSOT 60
QY 61 SDRPIEMKKIOBQTYVFFDNKIOGDLGRAEILIGKSLKIMNTVRDSALYRCEVVAR 120
DB 61 SDRPIEMKKIOBQTYVFFDNKIOGDLGRAEILIGKSLKIMNTVRDSALYRCEVVAR 120
QY 121 NDRKEIDELIVELTVQVKVPTVPCRVKPAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDELIVELTVQVKVPTVPCRVKPAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLSEGTGLVFTAVHKDQSGQYCIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSSHLSEGTGLVFTAVHKDQSGQYCIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGVLLVLAVALITLIGICAYRRGYFINNKODGESYKPKPGVNYIRTBEG 300
DB 241 NIGGIIGVLLVLAVALITLIGICAYRRGYFINNKODGESYKPKPGVNYIRTBEG 300
QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

RESULT 10

AAB80408
ID AAB80408 standard; protein; 310 AA.

AC AAB80408;

DT 24-APR-2001 (first entry)

DE Secreted protein encoded by gene #38.

KM Secreted protein; human; autoimmunity; hyperproliferation; cardiovascular;

KW cerebrovascular; infection; food.

OS Homo sapiens.

PN WO200107459-A1.

PD 01-FEB-2001.

PF 20-JUL-2000; 2000WO-US019735.

XX

PF 07-JUL-2000; 2000EP-00114089.
XX 08-JUL-1999; 95JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2001-524255/58.
DR N-PSDB; MAK94243.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
XX Claim 8; SEQ ID NO 2845; 1380bp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5' and 3' ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 310 AA;
Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-111;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCALPDPFFLLFRGCLIGAVNKSNNRPVQEFSEVLSCTIIDSQT 60
DB 1 MALRRPRLRLCALPDPFFLLFRGCLIGAVNKSNNRPVQEFSEVLSCTIIDSQT 60
QY 61 SDPRIEMWKIODEQTYTFPDKTIQGLAGRAELIGTSLKINWTRDSDALYRCEVVAR 120
DB 61 SDPRIEMWKIODEQTYTFPDKTIQGLAGRAELIGTSLKINWTRDSDALYRCEVVAR 120
QY 121 NDRKEIDIVIELTVQVQVTPVCRVPKAVGKATLHCSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDIVIELTVQVQVTPVCRVPKAVGKATLHCSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANRFRNNSSHNSETGTLVFTAVHKDSDGQYTCIASNDAGSARCEDEMEYIDL 240
DB 181 PTDSRANRFRNNSSHNSETGTLVFTAVHKDSDGQYTCIASNDAGSARCEDEMEYIDL 240
QY 241 NIGGIGVLLVLAALITLGICAVARGYFINNKDGGESYKPGPDGNYRTDDEG 300
DB 241 NIGGIGVLLVLAALITLGICAVARGYFINNKDGGESYKPGPDGNYRTDDEG 300
QY 301 DFRHKSFFVI 310
DB 301 DFRHKSFFVI 310
RESULT 8
AAU12440 standard; protein; 310 AA.
AAU12440;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human PRO1868 polypeptide sequence.
XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.
XX
OS Homo sapiens.
XX
XX WO200140466-A2.
XX
XX 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
XX 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 24-FEB-2000; 2000WO-US005601.
PR 01-MAR-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000US-0187202P.
PR 03-MAR-2000; 2000WO-US006319.
PR 10-MAR-2000; 2000WO-US006884.
PR 15-MAR-2000; 2000WO-US007377.
PR 20-MAR-2000; 2000WO-US007532.
PR 21-MAR-2000; 2000WO-US008439.
PR 30-MAR-2000; 2000WO-US013705.
PR 17-MAY-2000; 2000WO-US014042.
PR 22-MAY-2000; 2000WO-US014941.
PR 30-MAY-2000; 2000WO-US015264.
PR 02-JUN-2000; 2000US-0209832P.
PR 05-JUN-2000; 2000WO-US020710.
PR 28-JUL-2000; 2000WO-US022031.
PR 11-AUG-2000; 2000WO-US023532.
PR 23-AUG-2000; 2000WO-US023328.
PR 24-AUG-2000; 2000WO-US030952.
PR 08-NOV-2000; 2000WO-US030973.
PR 10-NOV-2000; 2000WO-US030973.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood W, Zhang Z;
XX
XX WPI: 2001-408281/43.
DR N-PSDB; AAS21512.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
XX Claim 12; Fig 538; 813bp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO

XX PS Claim 1, Fig 124; 393pp; English.

CC The present sequence is one of sixty one novel secreted and transmembrane

CC PRO polypeptides. The PRO polypeptides are useful for treating skin

CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),

CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative

CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,

CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,

CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory

CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),

CC infertility, AIDS and diabetes and retinal disorders such as retinitis

CC pigmentosa. The PRO nucleic acids have applications in molecular

CC biology, including use as hybridization probes, and in chromosome and

CC gene mapping

XX SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 8.6e-131;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTVPVQEFSEVELSCITITDSQT 60

DB 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTVPVQEFSEVELSCITITDSQT 60

QY 61 SDPRIEMKKIODEQTYVFFDNKIQGDLAGRAELIGKTSIKIMWVTRDSALYRCEVVAR 120

DB 61 SDPRIEMKKIODEQTYVFFDNKIQGDLAGRAELIGKTSIKIMWVTRDSALYRCEVVAR 120

QY 121 NDRKEIDELIVELTVQVAPVTPVCRVPKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180

DB 121 NDRKEIDELIVELTVQVAPVTPVCRVPKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEQEMEYVDL 240

DB 181 PTDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEQEMEYVDL 240

QY 241 NIGGIIGVLLVLAVALITLIGICCAVRGYFINNKQDGSYKPKGPDGVNVIKRTDEEG 300

DB 241 NIGGIIGVLLVLAVALITLIGICCAVRGYFINNKQDGSYKPKGPDGVNVIKRTDEEG 300

QY 301 DFRHKSFEVI 310

DB 301 DFRHKSFEVI 310

RESULT 6

AAM93905

ID AAM93905 standard; protein; 310 AA.

AC AAM93905;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 4051.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

XX EPI130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI: 2001-524255/58.

DR N-PSDB; AAK94867.

XX 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

PS Claim 8; SEQ ID NO 4051, 1380pp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been isolated

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full

CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special

CC methods. The present sequence is a polypeptide encoded by a full length

CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM

CC format directly from EPO

XX SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 8.6e-131;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTVPVQEFSEVELSCITITDSQT 60

DB 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTVPVQEFSEVELSCITITDSQT 60

QY 61 SDPRIEMKKIODEQTYVFFDNKIQGDLAGRAELIGKTSIKIMWVTRDSALYRCEVVAR 120

DB 61 SDPRIEMKKIODEQTYVFFDNKIQGDLAGRAELIGKTSIKIMWVTRDSALYRCEVVAR 120

QY 121 NDRKEIDELIVELTVQVAPVTPVCRVPKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180

DB 121 NDRKEIDELIVELTVQVAPVTPVCRVPKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEQEMEYVDL 240

DB 181 PTDSRANPRFRNSSSHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEQEMEYVDL 240

QY 241 NIGGIIGVLLVLAVALITLIGICCAVRGYFINNKQDGSYKPKGPDGVNVIKRTDEEG 300

DB 241 NIGGIIGVLLVLAVALITLIGICCAVRGYFINNKQDGSYKPKGPDGVNVIKRTDEEG 300

QY 301 DFRHKSFEVI 310

DB 301 DFRHKSFEVI 310

RESULT 7

AAM93323

ID AAM93323 standard; protein; 310 AA.

AC AAM93323;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 2845.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

XX EPI130094-A2.

PD 05-SEP-2001.

QY 181 PTDSPANRFRNSSSHLNSETGTLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEYVDL 240
 DB 181 PTDSPANRFRNSSSHLNSETGTLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEYVDL 240
 QY 241 NIGGIIGVAVLAVLALITIGICCAVARGYFINNKDGSYKPGKPDGVNRYIRTDDEG 300
 DB 241 NIGGIIGVAVLAVLALITIGICCAVARGYFINNKDGSYKPGKPDGVNRYIRTDDEG 300
 QY 301 DFRHKSFEVI 310
 DB 301 DFRHKSFEVI 310
 RESULT 4
 AAB27276
 ID AAB27276 standard; protein; 310 AA.
 AC AAB27276;
 DT 23-FEB-2001 (first entry)
 DE Human confluency regulated adhesion molecule 1 #2.
 XX Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
 KM inflammation; cancer; wound; angiogenesis; human;
 KM confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
 XX Homo sapiens.
 OS WO200053749-A2.
 EN 14-SEP-2000.
 PD 13-MAR-2000; 2000WO-EP002219.
 PF 11-MAR-1999; 99EP-00200746.
 PR (RMPD-) RMP DICTAGENE SA.
 PA Imhof BA, Aurand-Lions M;
 PI WPI; 2000-587436/55.
 DR N-PSDB; AAA95306.
 XX Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
 PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
 FT reactions and modulating vascular permeability.
 PS Claim 2; Fig 6; 59p; English.
 CC The present sequence is the human confluency regulated adhesion molecule
 CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
 CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
 CC and coding sequence can be used in the treatment of cancer, inflammation,
 CC to modulate cell-cell interactions and angiogenesis, and in the
 CC modulation of wound healing
 XX
 SQ Sequence 310 AA;
 Query Match 99.6%; Score 1629; DB 3; Length 310;
 Best Local Similarity 99.7%; Freq. No. 8.6e-131;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MALRRPPLRLCARLPDPFLLFRGCLIGAVNKSNRTPVQEFSEVELSCIITDSQT 60
 DB 1 MALRRPPLRLCARLPDPFLLFRGCLIGAVNKSNRTPVQEFSEVELSCIITDSQT 60
 QY 61 SDPRLEWKKIQDEQTYTFPNKIQGLAGRAELIGKTSKINAVTRRDSALYRCEVVAR 120
 DB 61 SDPRLEWKKIQDEQTYTFPNKIQGLAGRAELIGKTSKINAVTRRDSALYRCEVVAR 120
 QY 61 SDPRLEWKKIQDEQTYTFPNKIQGLAGRAELIGKTSKINAVTRRDSALYRCEVVAR 120
 DB 61 SDPRLEWKKIQDEQTYTFPNKIQGLAGRAELIGKTSKINAVTRRDSALYRCEVVAR 120
 QY 121 NDRKIDIVIELTVQVCPVTPVCRVPAVPGKATLHCQESGHRPRHYSWRNDVPL 180
 DB 121 NDRKIDIVIELTVQVCPVTPVCRVPAVPGKATLHCQESGHRPRHYSWRNDVPL 180

DB 121 NDRKIDIVIELTVQVCPVTPVCRVPAVPGKATLHCQESGHRPRHYSWRNDVPL 180
 QY 181 PTDSPANRFRNSSSHLNSETGTLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEYVDL 240
 DB 181 PTDSPANRFRNSSSHLNSETGTLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEYVDL 240
 QY 241 NIGGIIGVAVLAVLALITIGICCAVARGYFINNKDGSYKPGKPDGVNRYIRTDDEG 300
 DB 241 NIGGIIGVAVLAVLALITIGICCAVARGYFINNKDGSYKPGKPDGVNRYIRTDDEG 300
 QY 301 DFRHKSFEVI 310
 DB 301 DFRHKSFEVI 310
 RESULT 5
 AAB80272
 ID AAB80272 standard; protein; 310 AA.
 AC AAB80272;
 DT 24-APR-2001 (first entry)
 DE Human PRO1868 protein.
 XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KM antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
 KM antiangiogenic; vasotrophic; antiasthmatic; antirheumatic; cancer;
 KM antiarthritis; antiinfectivity; antidiabetic; antiviral; diabetes;
 KM ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KM ischaemia; inflammation.
 XX Homo sapiens.
 OS WO200104311-A1.
 EN 18-JAN-2001.
 PD 22-FEB-2000; 2000WO-US004414.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Botstein D, Deenoyers L, Eaton DL, Ferrara N,
 PI Filvaroft E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godcowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin J,
 PI Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WJ;
 DR WPI; 2001-081051/09.
 N-PSDB; AAF72433.
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).

QY 61 SDPRLEWKKIODEQTTVYFEDNKIQGDLGRAEILGKTSIKIWNTRDPSALYRCEVAV 120
 Db 61 SDPRLEWKKIODEQTTVYFEDNKIQGDLGRAEILGKTSIKIWNTRDPSALYRCEVAV 120
 QY 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180
 Db 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180
 QY 181 PTDSRANPRFRNSSHNLNSETGLVFTAVKDDSGOYYCIASNDAGSARCEQEMEVYDL 240
 Db 181 PTDSRANPRFRNSSHNLNSETGLVFTAVKDDSGOYYCIASNDAGSARCEQEMEVYDL 240
 QY 241 NIGGIIGGVVLAVALITLIGICCAVRGVTINNODGSSYKPKPGVNVIRFDEBG 300
 Db 241 NIGGIIGGVVLAVALITLIGICCAVRGVTINNODGSSYKPKPGVNVIRFDEBG 300
 QY 301 DFRKSSFVI 310
 Db 301 DFRKSSFVI 310
 Db 301 DFRKSSFVI 310
 RESULT 3
 AAB33457
 ID AAB33457 standard; protein; 310 AA.
 AC AAB33457;
 XX 29-JAN-2001 (first entry)
 DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
 XX Human: immune related disease; diagnosis; antiinflammatory; cardiac;
 KW dermatological; antihypertensive; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;
 KW antianemic; hepatotropic; vitruide; antipruritic; antiallergic;
 KW antiautismic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX Homo sapiens.
 OS
 XX WO200053758-A2.
 XX 14-SEP-2000.
 PF 02-MAR-2000; 2000WO-US005841.
 XX 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99WO-US012252.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145696P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162508P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030099.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AJ, Hebert C, Henzel W,
 PI Kabakoff RC, Lu Y, Pan Y, Penica D, Shelton DL, Smith V,
 PI Stewart TA, Tumas D, Watanabe CK, Wood WJ, Yan M;
 XX WPI: 2000-572271/53.
 DR N-PSDB; AAC58622.
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 PS Claim 33; Fig 88; 309pp; English.
 XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic
 CC disease, immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC5837 to AAC5857
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC5857 to AAC5864 and AAB3341 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 310 AA;
 QY Query Match 99.6%; Score 1629; DB 3; Length 310;
 Db Best Local Similarity 99.7%; Pred. No. 8.6e-131;
 QY Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MALRRPRLRLCARLDPDFLLILFRGCLIGAVNLKSNRTVPVOCFSEVSELCITTDQ 60
 QY 1 MALRRPRLRLCARLDPDFLLILFRGCLIGAVNLKSNRTVPVOCFSEVSELCITTDQ 60
 Db 61 SDPRLEWKKIODEQTTVYFEDNKIQGDLGRAEILGKTSIKIWNTRDPSALYRCEVAV 120
 QY 61 SDPRLEWKKIODEQTTVYFEDNKIQGDLGRAEILGKTSIKIWNTRDPSALYRCEVAV 120
 Db 61 SDPRLEWKKIODEQTTVYFEDNKIQGDLGRAEILGKTSIKIWNTRDPSALYRCEVAV 120
 QY 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180
 Db 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180
 QY 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180
 Db 121 NDKREIDEIVIELTVQVAVTPVCRVPAVPGKMATLHCQSESGHPRPHYSWYNDVPL 180

XX Claim 1, Page 82-83; 105pp; English.

PS The present sequence is the human immunoglobulin superfamily protein

XX IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is

CC expressed in reproductive, nervous and cardiovascular tissue, where

CC cancer and inflammation are common. The gene, protein, its antibodies,

CC agonists and antagonists are suitable for diagnosing and treating many

CC diseases, including cancer, immune system disorders (such as

CC inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,

CC atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,

CC emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,

CC rheumatoid arthritis, scleroderma, systemic lupus erythematosus and

CC ulcerative colitis), complications of cancer, haemodialysis and

CC extracorporeal circulation, trauma and haematopoietic cancer (such as

CC leukaemia) and infections caused by bacteria, viruses, fungi or parasites

XX

Sequence 310 AA:

Query Match 100.0%; Score 1635; DB 3; Length 310;

Best Local Similarity 100.0%; Pred. No. 2.7e-131;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSQT 60

DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSQT 60

QY 61 SDPRIEMWKIODEQTYVFFDNKIQGDLAGAEILGKTSIKINVTSRDSALYRCEVVAR 120

DB 61 SDPRIEMWKIODEQTYVFFDNKIQGDLAGAEILGKTSIKINVTSRDSALYRCEVVAR 120

QY 121 NDRKEIDIVIELTVOQVPRVPRVAVGVGKATLHCQESGHPHYSWVRNDVPL 180

DB 121 NDRKEIDIVIELTVOQVPRVPRVAVGVGKATLHCQESGHPHYSWVRNDVPL 180

QY 121 NDRKEIDIVIELTVOQVPRVPRVAVGVGKATLHCQESGHPHYSWVRNDVPL 180

DB 121 NDRKEIDIVIELTVOQVPRVPRVAVGVGKATLHCQESGHPHYSWVRNDVPL 180

QY 181 PTDSRANRPNSSSHLNSGTGLVFTAVHKDSCQVYCIASNDAGSARCEQMEVYDL 240

DB 181 PTDSRANRPNSSSHLNSGTGLVFTAVHKDSCQVYCIASNDAGSARCEQMEVYDL 240

QY 241 NIGGIGGVVVLAVLATITGICAYRGRFFINNKODGESYKPKGPDGNYRTDEEG 300

DB 241 NIGGIGGVVVLAVLATITGICAYRGRFFINNKODGESYKPKGPDGNYRTDEEG 300

QY 301 DFRHKSFEVI 310

DB 301 DFRHKSFEVI 310

RESULT 2

AA96735

ID AAY96735 standard; protein; 310 AA.

XX

AC AAY96735;

XX

DI 26-SEP-2000 (first entry)

XX

DE PRO1868, an A33 antigen homologue.

XX

KW PRO1868; A33 antigen; secreted protein; transmembrane protein;

XX anti-inflammatory; cytostatic; recombinant production; gene therapy.

OS Homo sapiens.

XX

FH Key

FT Peptide

FT 1. .30 Location/Qualifiers

FT /label= "Signal_peptide

FT 26. .31

FT /note= "N-myristoylation site"

FT 69. .77

FT /note= "Tyrosine kinase phosphorylation site"

FT 104. .107

FT /note= "N-glycosylation site"

FT 106. .109

FT Modified-site

FT /note= "Casein kinase II phosphorylation site"

FT 107. .110

FT /note= "cAMP- and cGMP-dependent protein kinase

FT phosphorylation site"

FT 192. .195

FT /note= "N-glycosylation site"

FT 215. .220

FT /note= "N-myristoylation site"

FT 226. .231

FT /note= "N-myristoylation site"

FT 243. .263

FT /label= "Transmembrane_domain

FT 243. .248

FT /note= "N-myristoylation site"

FT 244. .249

FT /note= "N-myristoylation site"

FT 262. .267

FT /note= "N-myristoylation site"

FT 296. .299

FT /note= "Casein kinase II phosphorylation site"

XX

PD 22-JUN-2000.

XX

PN WO200036102-A2.

XX

PF 01-DEC-1999; 99WO-US028634.

XX

PR 16-DEC-1998; 98US-0112851P.

PR 16-DEC-1998; 98US-0113145P.

PR 22-DEC-1998; 98US-0115511P.

PR 12-JAN-1999; 99US-0115588P.

PR 12-JAN-1999; 99US-0115565P.

PR 12-JAN-1999; 99US-0115733P.

PR 09-FEB-1999; 98US-0119341P.

PR 10-FEB-1999; 98US-0118537P.

PR 12-FEB-1999; 98US-0119655P.

PR 02-JUN-1999; 99WO-US012252.

XX

PA (GENTH) GENENTECH INC.

XX

PI Botstein D, Desnovers L, Ferrara N, Fong S, Gao W, Goddard A;

PI Gurney AL, Pan U, Roy MA, Stewart TA, Thomas D, Watarabe CK;

PI Wood WI;

XX

DR WPI; 2000-431586/37.

XX

DR N-PSDB; AAA51265.

XX

PT Isolated nucleic acid molecule encodes a PRO polypeptide which is a

PT transmembrane polypeptide.

XX

PS Claim 1, Fig 14; 154pp; English.

XX

XX This is PRO1868, a putative homologue of A33 antigen, a known colorectal

CC cancer-associated marker. The invention concerns novel secreted and

CC transmembrane proteins, designated PRO polypeptides. The cDNA and gene

CC sequences are useful in the recombinant production of PRO polypeptides,

CC as a hybridization probe to screen libraries to isolate cDNAs with

CC sequence identity to PRO polypeptides or to map the gene encoding the PRO

CC polypeptides and analyzing genetic disorders. The cDNA/gene can also be

CC used to produce transgenic animals useful for the development and

CC screening of therapeutically useful reagents. They can also be used in

CC gene therapy, e.g. to replace a defective gene

XX

Sequence 310 AA:

Query Match 99.6%; Score 1629; DB 3; Length 310;

Best Local Similarity 99.7%; Pred. No. 8.6e-131;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSQT 60

DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSQT 60

APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/904,786
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 NUMBER OF SEQ ID NOS: 423
 SRO ID NO 423
 LENGTH: 310
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-904-786-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
 Best Local Similarity 99.7%; Pred. No. 9,6e-133;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTPVYQEFSEVELSCITDSQT 60
 DB 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTPVYQEFSEVELSCITDSQT 60
 QY 61 SDPRIEWKTIODEQTTVFFDNKIQGLAGRAEILGKSLKINVTTRDSALYRCEVAR 120
 DB 61 SDPRIEWKTIODEQTTVFFDNKIQGLAGRAEILGKSLKINVTTRDSALYRCEVAR 120
 QY 121 NDRKEIDEIVIELTVQVPEVTPVCRVPKAVPVGMATLHCQSESGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEIDEIVIELTVQVPEVTPVCRVPKAVPVGMATLHCQSESGHPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSSHINSETGLVFTAVHKDSDGOYYCIAANDAGSARCEQEMEVYDL 240
 DB 181 PTDSRANPRFRNSSSHINSETGLVFTAVHKDSDGOYYCIAANDAGSARCEQEMEVYDL 240
 QY 241 NIGGIIGVIVLAVLALITLIGICAVRGGYFINNKODGESYNPGKPDGVNVIIRTBEG 300
 DB 241 NIGGIIGVIVLAVLALITLIGICAVRGGYFINNKODGESYNPGKPDGVNVIIRTBEG 300
 QY 301 DFRKSSFEVI 310
 DB 301 DFRKSSFEVI 310

Search completed: April 12, 2004, 09:22:02
 Job time : 46 secs

QY 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKODGESYKNPKRPGVNYIRTDDEG 300
DB 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKODGESYKNPKRPGVNYIRTDDEG 300
QY 301 DFRKSSFVI 310
DB 301 DFRKSSFVI 310

RESULT 14
US-09-904-820-423
Sequence 423, Application US/09904820
Publication No. US20030036094A1
GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,820
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-820-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9, 6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLILLFRGCLIGAVNLKSSNRTPVVOEFESVELSCITTDSDT 60
DB 1 MALRRPRLRLCARLPDPFLILLFRGCLIGAVNLKSSNRTPVVOEFESVELSCITTDSDT 60
QY 61 SDRRIEMKKIODEQTTVFEDNKIQGDLGRAEIIIGKTSLSKIWNVTRRDSALYRCGVAR 120
DB 61 SDRRIEMKKIODEQTTVFEDNKIQGDLGRAEIIIGKTSLSKIWNVTRRDSALYRCGVAR 120
QY 121 NDRKEIDELVIEITVQVKRVTVCVRPKAVPVGKATLHCQSEBGRPHYSMYRNDVPL 180
DB 121 NDRKEIDELVIEITVQVKRVTVCVRPKAVPVGKATLHCQSEBGRPHYSMYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHINSETGLVFTAVHKDQSGGYCIAASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFRNSSSHINSETGLVFTAVHKDQSGGYCIAASNDAGSARCEQMEVYDL 240
QY 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKODGESYKNPKRPGVNYIRTDDEG 300
DB 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKODGESYKNPKRPGVNYIRTDDEG 300
QY 301 DFRKSSFVI 310
DB 301 DFRKSSFVI 310

RESULT 15
US-09-904-786-423
Sequence 423, Application US/09904786
Publication No. US2003003969A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey

Mon Apr 12 09:42:29 2004

us-09-831-805a-6.rapb

Page 10

PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-859-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALRRPRLRLCARLPDFLLFRGLIGAVNKKSNRTPVQEFSEVLSCTITDSQT 60
1 MALRRPRLRLCARLPDFLLFRGLIGAVNKKSNRTPVQEFSEVLSCTITDSQT 60
61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSIKINWTRRDSALYCEVVAR 120
61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSIKINWTRRDSALYCEVVAR 120
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
181 PTDSRANPRFNSSSHNSSETGLVFTAVKXDSGQYTCIASNDAGSARCEQEMEYVDL 240
181 PTDSRANPRFNSSSHNSSETGLVFTAVKXDSGQYTCIASNDAGSARCEQEMEYVDL 240
241 NIGGIIGVTVLAVLALITIGICCAVRRGYFINNKGESYKNGKRDGVNVRTDEEG 300
241 NIGGIIGVTVLAVLALITIGICCAVRRGYFINNKGESYKNGKRDGVNVRTDEEG 300
241 NIGGIIGVTVLAVLALITIGICCAVRRGYFINNKGESYKNGKRDGVNVRTDEEG 300
301 DFRHKSFEVI 310
301 DFRHKSFEVI 310
Db

RESULT 13
US-09-909-204-423
Sequence 423, Application US/09909204
Publication No. US20030036061A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batson, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Rong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kunkel, Thomas J.

APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-204-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALRRPRLRLCARLPDFLLFRGLIGAVNKKSNRTPVQEFSEVLSCTITDSQT 60
1 MALRRPRLRLCARLPDFLLFRGLIGAVNKKSNRTPVQEFSEVLSCTITDSQT 60
61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSIKINWTRRDSALYCEVVAR 120
61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSIKINWTRRDSALYCEVVAR 120
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
121 NDRKEIDEIVIELTVQKPTVPCRVKAVPGKATLHCQESGHPHYSWYRNDVPL 180
181 PTDSRANPRFNSSSHNSSETGLVFTAVKXDSGQYTCIASNDAGSARCEQEMEYVDL 240
181 PTDSRANPRFNSSSHNSSETGLVFTAVKXDSGQYTCIASNDAGSARCEQEMEYVDL 240
241 NIGGIIGVTVLAVLALITIGICCAVRRGYFINNKGESYKNGKRDGVNVRTDEEG 300
241 NIGGIIGVTVLAVLALITIGICCAVRRGYFINNKGESYKNGKRDGVNVRTDEEG 300
301 DFRHKSFEVI 310
301 DFRHKSFEVI 310
Db

APPLICANT: Gerriksen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: 10466-14
 CURRENT FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 423
 LENGTH: 310
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-907-942-423
 Query Match 99.6%; Score 1629; DB 10; Length 310;
 Best Local Similarity 99.7%; Pred. No. 9.6e-133;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALRRPPLRLCALPPFLFLFRGLIGAVNKKSNRPVVOEFESVELSITIDSGT 60
 1 MALRRPPLRLCALPPFLFLFRGLIGAVNKKSNRPVVOEFESVELSITIDSGT 60
 61 SDPRLEWKKIODEQTTVFVFNKIQGLAGRAELIGKTSIKINVTTRRSALYRCCEVAR 120
 61 SDPRLEWKKIODEQTTVFVFNKIQGLAGRAELIGKTSIKINVTTRRSALYRCCEVAR 120

121 NDRKEIDEIVETLTQVKRVTVCGRVPAKVPVGRKATLHQSESGHPRPHYSWYNDVPL 180
 121 NDRKEIDEIVETLTQVKRVTVCGRVPAKVPVGRKATLHQSESGHPRPHYSWYNDVPL 180
 181 PTDSRANPRFRNSSSHLNSGTUFTAVHKDSDGOYCIASNDASARCECEMEVYDL 240
 181 PTDSRANPRFRNSSSHLNSGTUFTAVHKDSDGOYCIASNDASARCECEMEVYDL 240
 241 NIGGIIGVLTVALATLTLGICAYRRGTYTNKKDSESTKNGKPDGVNIRTDEBG 300
 241 NIGGIIGVLTVALATLTLGICAYRRGTYTNKKDSESTKNGKPDGVNIRTDEBG 300
 301 DFRHKSFFVI 310
 301 DFRHKSFFVI 310

RESULT 12
 US-09-904-859-423
 Sequence 423, Application US/09904859
 Publication No. US20030036060A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerriksen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: 10466-14
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214

Mon Apr 12 09:42:29 2004

us-09-831-805a-6.rapb

Page 8

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTFVQEFSEVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTFVQEFSEVELSCIITDSQT 60
QY 61 SDPRIRWKXIOBQOTTYVFDNKTIOGDLGRABITLKTSLKMTWTRDSALYRCEVVAR 120
Db 61 SDPRIRWKXIOBQOTTYVFDNKTIOGDLGRABITLKTSLKMTWTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQKVPYTCVAVKAVPVGKATLHCQESGHPRHYSWYENDVPL 180
Db 121 NDRKEIDEIVIELTVQKVPYTCVAVKAVPVGKATLHCQESGHPRHYSWYENDVPL 180
QY 181 PDSRANPRFRNSSSHINSEGTFTVTAHKDQSGQYICIASNDGASARCEQEMEYVDL 240
Db 181 PDSRANPRFRNSSSHINSEGTFTVTAHKDQSGQYICIASNDGASARCEQEMEYVDL 240
QY 241 NIGGIIIGVAVLAVLALITLIGICAVRRGYFINNKQDESYKNGKPDGVNVRTDEBG 300
Db 241 NIGGIIIGVAVLAVLALITLIGICAVRRGYFINNKQDESYKNGKPDGVNVRTDEBG 300
QY 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

RESULT 10
US-09-907-613-423
Sequence 423, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Godowski, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaud, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, T.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907, 613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23039
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-613-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9,6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTFVQEFSEVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTFVQEFSEVELSCIITDSQT 60
QY 61 SDPRIRWKXIOBQOTTYVFDNKTIOGDLGRABITLKTSLKMTWTRDSALYRCEVVAR 120
Db 61 SDPRIRWKXIOBQOTTYVFDNKTIOGDLGRABITLKTSLKMTWTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQKVPYTCVAVKAVPVGKATLHCQESGHPRHYSWYENDVPL 180
Db 121 NDRKEIDEIVIELTVQKVPYTCVAVKAVPVGKATLHCQESGHPRHYSWYENDVPL 180
QY 181 PDSRANPRFRNSSSHINSEGTFTVTAHKDQSGQYICIASNDGASARCEQEMEYVDL 240
Db 181 PDSRANPRFRNSSSHINSEGTFTVTAHKDQSGQYICIASNDGASARCEQEMEYVDL 240
QY 241 NIGGIIIGVAVLAVLALITLIGICAVRRGYFINNKQDESYKNGKPDGVNVRTDEBG 300
Db 241 NIGGIIIGVAVLAVLALITLIGICAVRRGYFINNKQDESYKNGKPDGVNVRTDEBG 300
QY 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

RESULT 11
US-09-907-942-423
Sequence 423, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter

PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20534
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLDPFLLILFRGCLIGAVNLKSNFTPVQEFSEVLSCTITDST 60
DB 1 MALRRPRLRLCARLDPFLLILFRGCLIGAVNLKSNFTPVQEFSEVLSCTITDST 60
QY 61 SDRIRIMWKIODEQOTTVVFPDNKIQDGLGRABILIGKTSIKIMVTRRDSALYRCEVAR 120
DB 61 SDRIRIMWKIODEQOTTVVFPDNKIQDGLGRABILIGKTSIKIMVTRRDSALYRCEVAR 120
QY 121 NDRKEIDEIVIELTVQKPYTPVCRAVPGKAVPGKATLHCQESSEGHPRPHYSYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKPYTPVCRAVPGKAVPGKATLHCQESSEGHPRPHYSYRNDVPL 180
QY 181 PTGSRANPRRNSSSHANSETGLVPTAATKDDSGGYCCIASDASACEQEMEVYVL 240
DB 181 PTGSRANPRRNSSSHANSETGLVPTAATKDDSGGYCCIASDASACEQEMEVYVL 240
QY 241 NIGGIIGVVLAVLALITLIGICAYRSGYFTNNKQDSYNNPKPGDGVNVIIRTEDEG 300
DB 241 NIGGIIGVVLAVLALITLIGICAYRSGYFTNNKQDSYNNPKPGDGVNVIIRTEDEG 300
QY 301 DFRHKSFEVI 310
DB 301 DFRHKSFEVI 310

RESULT 9
US-09-906-838-423
Sequence 423, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Publication No. US20030003530A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvarolf, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/904,011
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 423
 LENGTH: 310
 TYPE: PRT
 ORGANISM: Homo Sapien

US-09-904-011-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
 Best Local Similarity 99.7%; Pred. No. 9,6e-133;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAIRPPRLRLCARLPDFFLLIFRCGLIGAVNLKSSNTPVQEESEVLSGLITDSQT	60
DB	1	MAIRPPRLRLCARLPDFFLLIFRCGLIGAVNLKSSNTPVQEESEVLSGLITDSQT	60
QY	61	SDPRIEWKKIQDEQTVTFVFDNKRIOGDLGRABILLKTSIKINVTTRDSALYRCEVVAR	120
DB	61	SDPRIEWKKIQDEQTVTFVFDNKRIOGDLGRABILLKTSIKINVTTRDSALYRCEVVAR	120
QY	121	NDKREIDEIVIELTVQYKVPYPCRVKAVPVGKMTLHCQEESEGHPRPHYSWYRDDVPL	180
DB	121	NDKREIDEIVIELTVQYKVPYPCRVKAVPVGKMTLHCQEESEGHPRPHYSWYRDDVPL	180
QY	181	PTDSRANPRFNSSSHINSETGLVFTAVHAKDSDGQYVCIASNDAGSARCEQEMEYDL	240
DB	181	PTDSRANPRFNSSSHINSETGLVFTAVHAKDSDGQYVCIASNDAGSARCEQEMEYDL	240
QY	241	NIIGIGGLVLAVALITLIGICAVRGGFTINNKODGSESYNPKGPDGVNTRITDEEG	300
DB	241	NIIGIGGLVLAVALITLIGICAVRGGFTINNKODGSESYNPKGPDGVNTRITDEEG	300
QY	301	DFRHKSSFVI 310	
DB	301	DFRHKSSFVI 310	

RESULT 8
 US-09-906-742-423

Sequence 423, Application US/09906742

Publication No. US20030023054A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvarolf, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/906,742
 CURRENT FILING DATE: 2001-07-16
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698

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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-423

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Query Match          99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTPVQEFESVELSCITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSNRTPVQEFESVELSCITDSQT 60
QY 61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSKIMWTRDSALYRCEVVAR 120
DB 61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSKIMWTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGMATLHCOSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGMATLHCOSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDSDGQYCIASNDAGSARCEQEMEYVDL 240
DB 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDSDGQYCIASNDAGSARCEQEMEYVDL 240
QY 241 NIGGIIGVLYLVAVLALITLIGICAYRGGYFINNKODGESYKPKGXPQGVNYYRTDEEG 300
DB 241 NIGGIIGVLYLVAVLALITLIGICAYRGGYFINNKODGESYKPKGXPQGVNYYRTDEEG 300
QY 301 DFRHKSFFVI 310
DB 301 DFRHKSFFVI 310

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RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366a1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerstein, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.

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; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: US/09/907, 841
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-841-423

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Query Match          99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 SDPRIEWKKIODEQTYVFFDNKIQGLAGRAELIGKTSKIMWTRDSALYRCEVVAR 120
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DB 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGMATLHCOSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDSDGQYCIASNDAGSARCEQEMEYVDL 240
DB 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDSDGQYCIASNDAGSARCEQEMEYVDL 240
QY 241 NIGGIIGVLYLVAVLALITLIGICAYRGGYFINNKODGESYKPKGXPQGVNYYRTDEEG 300
DB 241 NIGGIIGVLYLVAVLALITLIGICAYRGGYFINNKODGESYKPKGXPQGVNYYRTDEEG 300
QY 301 DFRHKSFFVI 310
DB 301 DFRHKSFFVI 310

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RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011

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Mon Apr 12 09:42:29 2004

us-09-831-805a-6.rapb

Page 4

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-423

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61 SDPRLEWKKIODEQTTVYFNDKIOGDIAGRAEIIIGKTSKIMVTRSDSLHYCEVYAR 120
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121 NDRKEIDEIVIELTVQYKPTPVCRVPRKAVPVGKMATLHCQSESGHPRPHYSYRNDVPL 180
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181 PTDRANPRFRNSSSHNSRTGLVFAVHKDSCGYCYCIASNDAGSARCEOEVEYDL 240
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Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desrochers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214

QY 1 MALRRPRLRLCARLPDFFLLLLFRGCLLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT 60
1 MALRRPRLRLCARLPDFFLLLLFRGCLLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT 60
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61 SDRRIEMWKIODEQTYTFPFNKKIOGDLGRAELIKTSIKINVTTRDSALYCEVAR 120
Db 61 SDRRIEMWKIODEQTYTFPFNKKIOGDLGRAELIKTSIKINVTTRDSALYCEVAR 120
QY 121 NDRKEIDEIVIELTVQKPYTPVCRVPAVVGKMATLHCQESGHPHYSWYRNDVPL 180
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Db 121 NDRKEIDEIVIELTVQKPYTPVCRVPAVVGKMATLHCQESGHPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLNSETGTLVFAVHKDSDGQYCIASNDAGSARCEOEWEVYDL 240
181 PTDSRANPRFRNSSSHLNSETGTLVFAVHKDSDGQYCIASNDAGSARCEOEWEVYDL 240
Db 181 PTDSRANPRFRNSSSHLNSETGTLVFAVHKDSDGQYCIASNDAGSARCEOEWEVYDL 240
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241 NIGGIIIGVAVLAVLALITLIGICAYRGGYFINNKQGESYKNGPKPDGVNYIRTDSEG 300
Db 241 NIGGIIIGVAVLAVLALITLIGICAYRGGYFINNKQGESYKNGPKPDGVNYIRTDSEG 300
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RESULT 3
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905, 291A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-291A-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Freq. No. 9,6e-13;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MALRRPRLRLCARLPDFFLLLLFRGCLLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLLLFRGCLLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT 60
QY 61 SDRRIEMWKIODEQTYTFPFNKKIOGDLGRAELIKTSIKINVTTRDSALYCEVAR 120
61 SDRRIEMWKIODEQTYTFPFNKKIOGDLGRAELIKTSIKINVTTRDSALYCEVAR 120
Db 61 SDRRIEMWKIODEQTYTFPFNKKIOGDLGRAELIKTSIKINVTTRDSALYCEVAR 120
QY 121 NDRKEIDEIVIELTVQKPYTPVCRVPAVVGKMATLHCQESGHPHYSWYRNDVPL 180
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Db 121 NDRKEIDEIVIELTVQKPYTPVCRVPAVVGKMATLHCQESGHPHYSWYRNDVPL 180
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181 PTDSRANPRFRNSSSHLNSETGTLVFAVHKDSDGQYCIASNDAGSARCEOEWEVYDL 240
Db 181 PTDSRANPRFRNSSSHLNSETGTLVFAVHKDSDGQYCIASNDAGSARCEOEWEVYDL 240
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Sequence 423, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter

PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 2
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Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Mon Apr 12 09:42:29 2004

us-09-831-805a-6.rapb

Page 1

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15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	99.6	310	US-09-909-320-423	Sequence 423, App
2	1629	99.6	310	US-09-909-088B-423	Sequence 423, App
3	1629	99.6	310	US-09-905-291A-423	Sequence 423, App
4	1629	99.6	310	US-09-902-853-423	Sequence 423, App
5	1629	99.6	310	US-09-907-824-423	Sequence 423, App
6	1629	99.6	310	US-09-907-841-423	Sequence 423, App
7	1629	99.6	310	US-09-904-011-423	Sequence 423, App
8	1629	99.6	310	US-09-906-742-423	Sequence 423, App
9	1629	99.6	310	US-09-906-838-423	Sequence 423, App
10	1629	99.6	310	US-09-907-613-423	Sequence 423, App
11	1629	99.6	310	US-09-907-942-423	Sequence 423, App
12	1629	99.6	310	US-09-904-859-423	Sequence 423, App
13	1629	99.6	310	US-09-909-204-423	Sequence 423, App
14	1629	99.6	310	US-09-904-820-423	Sequence 423, App
15	1629	99.6	310	US-09-904-786-423	Sequence 423, App

15	1629	99.6	310	10	US-09-906-646-423	Sequence 423, App
17	1629	99.6	310	10	US-09-906-700-423	Sequence 423, App
18	1629	99.6	310	10	US-09-903-786-423	Sequence 423, App
19	1629	99.6	310	10	US-09-902-903-423	Sequence 423, App
20	1629	99.6	310	10	US-09-903-749A-423	Sequence 423, App
21	1629	99.6	310	10	US-09-904-119-423	Sequence 423, App
22	1629	99.6	310	10	US-09-904-956-423	Sequence 423, App
23	1629	99.6	310	10	US-09-902-735-423	Sequence 423, App
24	1629	99.6	310	10	US-09-907-794-423	Sequence 423, App
25	1629	99.6	310	10	US-09-903-943-423	Sequence 423, App
26	1629	99.6	310	10	US-09-904-462-423	Sequence 423, App
27	1629	99.6	310	10	US-09-907-925-423	Sequence 423, App
28	1629	99.6	310	10	US-09-902-620-423	Sequence 423, App
29	1629	99.6	310	10	US-09-903-520-423	Sequence 423, App
30	1629	99.6	310	10	US-09-905-056-423	Sequence 423, App
31	1629	99.6	310	10	US-09-909-064-423	Sequence 423, App
32	1629	99.6	310	10	US-09-904-553-423	Sequence 423, App
33	1629	99.6	310	10	US-09-905-811-423	Sequence 423, App
34	1629	99.6	310	10	US-09-905-088-423	Sequence 423, App
35	1629	99.6	310	10	US-09-907-575-423	Sequence 423, App
36	1629	99.6	310	10	US-09-905-075-423	Sequence 423, App
37	1629	99.6	310	10	US-09-902-759-423	Sequence 423, App
38	1629	99.6	310	10	US-09-902-534-423	Sequence 423, App
39	1629	99.6	310	10	US-09-902-713-423	Sequence 423, App
40	1629	99.6	310	10	US-09-907-979-423	Sequence 423, App
41	1629	99.6	310	10	US-09-902-615-423	Sequence 423, App
42	1629	99.6	310	10	US-09-903-925-423	Sequence 423, App
43	1629	99.6	310	10	US-09-906-760A-423	Sequence 423, App
44	1629	99.6	310	10	US-09-903-823-423	Sequence 423, App
45	1629	99.6	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1

US-09-909-320-423

Sequence 423, Application US/0909320

Patent No. US20020132240A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Katon, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gertlisen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kijavlin, Iyar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

FILE REFERENCE: P1216R1 (US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match 25.6%; Score 419; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 8,4e-35;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

QY 8 RRLRCALPDPFLLFRGLIGAVNLKSNRTPVQEFESVLSCLITDSQSDPRIEW 67
DB 9 RKLCL----FILATLCSIALGSLVHSSEPEVRIPENNPKLSCAY--SGFSSPVEW 62
QY 68 KKIODEQTTVPFNDKIQGLDLAGRAELIGKTSKIMNWTNRDSALYRCEVAANDRKEID 127
DB 63 KFDGDTTRLVCYNNKKTASYEDRVFTL-PTGITPKSVTRDGTGYTC-MVSEBGSNSYG 120
QY 128 EIVELTYQVKPVTVCRAVPVGMATLHCOESGHRPHYSWYRNDVPLPTDSRAN 187
DB 121 EVKVKLIVLPSPKPTVINPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 180
QY 188 PRFNSSSHNSEGTIVFTAVHKDSDGOYCIASNDGASARCEQ-EMEYVDLNIIGII 246
DB 181 RAFNSSSVYLNPTTGLVFDPLSDTGEYSCEARNYGTPTMSNAVMEAVERNVGVIV 240
QY 247 GGVLVLAVALITLIGICCAVRGFIYNNKODGES---YKNPKGPDGVNIYRTDEGDF 302
DB 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKTSKKVIYSOPS-----ARSEGEF 291
QY 303 RHKSSFVI 310
DB 292 KQTSSFLV 299

RESULT 13
US-09-312-283C-189
Sequence 189, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated from skin cells
FILE REFERENCE: 11000,1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-189
Query Match 25.6%; Score 419; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 8,4e-35;

Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;
QY 8 RRLRCALPDPFLLFRGLIGAVNLKSNRTPVQEFESVLSCLITDSQSDPRIEW 67
DB 9 RKLCL----FILATLCSIALGSLVHSSEPEVRIPENNPKLSCAY--SGFSSPVEW 62
QY 68 KKIODEQTTVPFNDKIQGLDLAGRAELIGKTSKIMNWTNRDSALYRCEVAANDRKEID 127
DB 63 KFDGDTTRLVCYNNKKTASYEDRVFTL-PTGITPKSVTRDGTGYTC-MVSEBGSNSYG 120
QY 128 EIVELTYQVKPVTVCRAVPVGMATLHCOESGHRPHYSWYRNDVPLPTDSRAN 187
DB 121 EVKVKLIVLPSPKPTVINPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 180
QY 188 PRFNSSSHNSEGTIVFTAVHKDSDGOYCIASNDGASARCEQ-EMEYVDLNIIGII 246
DB 181 RAFNSSSVYLNPTTGLVFDPLSDTGEYSCEARNYGTPTMSNAVMEAVERNVGVIV 240
QY 247 GGVLVLAVALITLIGICCAVRGFIYNNKODGES---YKNPKGPDGVNIYRTDEGDF 302
DB 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKTSKKVIYSOPS-----ARSEGEF 291
QY 303 RHKSSFVI 310
DB 292 KQTSSFLV 299

RESULT 14
US-09-312-283C-331
Sequence 331, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated from skin cells
FILE REFERENCE: 11000,1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-331

Query Match 25.6%; Score 419; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 8,4e-35;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;
QY 8 RRLRCALPDPFLLFRGLIGAVNLKSNRTPVQEFESVLSCLITDSQSDPRIEW 67
DB 9 RKLCL----FILATLCSIALGSLVHSSEPEVRIPENNPKLSCAY--SGFSSPVEW 62
QY 68 KKIODEQTTVPFNDKIQGLDLAGRAELIGKTSKIMNWTNRDSALYRCEVAANDRKEID 127
DB 63 KFDGDTTRLVCYNNKKTASYEDRVFTL-PTGITPKSVTRDGTGYTC-MVSEBGSNSYG 120
QY 128 EIVELTYQVKPVTVCRAVPVGMATLHCOESGHRPHYSWYRNDVPLPTDSRAN 187
DB 121 EVKVKLIVLPSPKPTVINPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 180
QY 188 PRFNSSSHNSEGTIVFTAVHKDSDGOYCIASNDGASARCEQ-EMEYVDLNIIGII 246
DB 181 RAFNSSSVYLNPTTGLVFDPLSDTGEYSCEARNYGTPTMSNAVMEAVERNVGVIV 240
QY 247 GGVLVLAVALITLIGICCAVRGFIYNNKODGES---YKNPKGPDGVNIYRTDEGDF 302

TYPE: PRT
ORGANISM: Mus musculus
US-09-254-465A-10

Query Match 27.5%; Score 449.5; DB 4; Length 300;
Best Local Similarity 35.2%; Pred. No. 6.1e-38;
Matches 105; Conservative 56; Mismatches 122; Indels 15; Gaps 7;

20 LLLFPGCLIGAV-----MLKSNRPVVOEFSEVELSCITIDSCISDPRIMKQIODEQ 74
11 LLLFPGCLIGAV-----MLKSNRPVVOEFSEVELSCITIDSCISDPRIMKQIODEQ 68
75 TTYVFPDNKIQDGLAGRAELIGKTSIKINVTNRDSALYRCEVVAANDKEIDEIVIELT 134
69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGQNYGEVSIHLT 126
135 VOYKPTVPVCRVPRKAVPVGKATLHCOESGHRPHYSWYRNDVPLPT-DSRANPFRS 193
127 VLVPSKPTISVSSVTIGRAVLTCSHDSPSEYSWFKDISMLTDKKTAFAMNS 186
194 SSHLNSETGLVFTAVHKDSDGOYTCIASNDAGSA-RCEQEMEVYDNLNGIIGVLV 252
187 SFTIDPSGDLIFDPVTAFFDSGEYCOAQNGYGTARSEAAHMDAVELNNGIIVAVLT 246
253 LAVVALITLIGICAVRGYFINKKODGESYKRNPKGPDGVNVIITDESGDPRHKSFEI 310
247 LILGLLIFGVWPAVSKGYFTTKG---TAPGKVIVSQPSTRSGEFGKOTSEFLV 300

RESULT 10
US-09-188-930-331
Sequence 331, Application US/09188930A

Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011C1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Human
US-09-188-930-331

Query Match 25.6%; Score 419; DB 3; Length 299;

Best Local Similarity 32.8%; Pred. No. 8.4e-35;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

8 RLRLCARLPDPFLLLFPGCLIGAVNLKSNRPVVOEFSEVELSCITIDSCISDPRIM 67
9 RLRLCL-----FLAILLCSLALGSVTVASSEPEVRIPENNFKLSQAY--SGFSSPVEW 62
68 KKIODEQTYVFPDNKIQDGLAGRAELIGKTSIKINVTNRDSALYRCEVVAANDKEID 127
63 KFDGDTIRLVQYNNKKTASTYEDRTPL-PGITPKSVTRDGTGYTC-MVSEEGNSYG 120
128 EIVIELTVQKRVTPVCRVPRKAVPVGKATLHCOESGHRPHYSWYRNDVPLPTDSRAN 187
121 EVKVLIVLVPPSKPTVNI PSSATIGNRAVLTCSHDSPSEYSWFKDISMLTDKKTAFAMNS 180
186 PRFRSSSHLNSETGLVFTAVHKDSDGOYTCIASNDAGSARCEQ-EMEVYDNLNGII 246
181 RAFNSSSVYLNPTTBELVFDPLASDTGEYSCERANGYGTPTSTNAVMEAVERNVAVIY 240
247 GGVLVAVLAVLITLIGICAVRGYFINKKODGES---YKPKGPDGVNVIITDESGDF 302

241 AAVLVTLILGILVGFVWPAVSKGYFTTKG---TAPGKVIVSQPSTRSGEFGKOTSEFLV 291
303 RHKSSFEI 310
292 KOTSSFEI 299

RESULT 11
US-09-462-270-2
Sequence 2, Application US/09462270

Patent No. 6358707
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Human P1 Antigen: A Cell Surface
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 299
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match 25.6%; Score 419; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 8.4e-35;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

8 RLRLCARLPDPFLLLFPGCLIGAVNLKSNRPVVOEFSEVELSCITIDSCISDPRIM 67
9 RLRLCL-----FLAILLCSLALGSVTVASSEPEVRIPENNFKLSQAY--SGFSSPVEW 62
68 KKIODEQTYVFPDNKIQDGLAGRAELIGKTSIKINVTNRDSALYRCEVVAANDKEID 127
63 KFDGDTIRLVQYNNKKTASTYEDRTPL-PGITPKSVTRDGTGYTC-MVSEEGNSYG 120
128 EIVIELTVQKRVTPVCRVPRKAVPVGKATLHCOESGHRPHYSWYRNDVPLPTDSRAN 187
121 EVKVLIVLVPPSKPTVNI PSSATIGNRAVLTCSHDSPSEYSWFKDISMLTDKKTAFAMNS 180
186 PRFRSSSHLNSETGLVFTAVHKDSDGOYTCIASNDAGSARCEQ-EMEVYDNLNGII 246
181 RAFNSSSVYLNPTTBELVFDPLASDTGEYSCERANGYGTPTSTNAVMEAVERNVAVIY 240
247 GGVLVAVLAVLITLIGICAVRGYFINKKODGES---YKPKGPDGVNVIITDESGDF 302
241 AAVLVTLILGILVGFVWPAVSKGYFTTKG---TAPGKVIVSQPSTRSGEFGKOTSEFLV 291
303 RHKSSFEI 310
292 KOTSSFEI 299

RESULT 12
US-09-254-465A-1
Sequence 1, Application US/09254465A

Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT OF DISEASES CHARACTERIZED BY A3-RELATED ANTIGENS

Mon Apr 12 09:42:28 2004

us-09-831-805a-6.rat

Page 6

Db 51 -KTPKTVSSRLKMKL-GRSVSVFYVQOTLQDGFKNRLEM-DFNIRIKNTRSDAGKY 107
Qy 114 RCEVVAANDR-KEIDIEYIELTVQKPYTPVCSVPKAVVGMKATLHCQSEEGHPRPHYS 172
Db 108 RCEVVAAPSEGGQLEEDTVLETVAPVAPVSCVPSALSGTVLRCQDKGPNAPERYT 167
Qy 173 WYRNDVPLPTDSRANPRFRNSSHNLSEGTGLVFAVHKDSCGYCTASNDAGSARCEE 232
Db 168 WFKDGRILLENPRLSQSTNSSYMNTKTGTLQFNVTSSKLDGTGEYSCEARNVSVGRCPG 227
Qy 233 OMEVYDINIGTIGGVLVVALITLITGICAYRGYF 272
Db 228 KRMQVDDINISGIIAAVVVALVSVCGLGVCYARQKGYF 267

RESULT 8
US-09-902-775A-64
Sequence 64, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvarolf, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30939
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-64
Query Match 27.9%; Score 456.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 1.2e-36;
Matches 104; Conservative 51; Mismatches 104; Indels 21; Gaps 7;
Qy 1 MALRRPRLRCALPDEFILLFRGLIG-----AVNLSSNRPVQ--EFESVEISC 53
Db 1 MARSRRL-----LILLRLVVALGYHKAVGFSAKQGVTVAVTEGAILAC 50
Qy 54 IITDSQSDPRIEMWKLODEQTYVFPDNKIQDLAGRAELIGTSKINVTTRDSALY 113
Db 51 -KTPKTVSSRLKMKL-GRSVSVFYVQOTLQDGFKNRLEM-DFNIRIKNTRSDAGKY 107
Qy 114 RCEVVAANDR-KEIDIEYIELTVQKPYTPVCSVPKAVVGMKATLHCQSEEGHPRPHYS 172
Db 108 RCEVVAAPSEGGQLEEDTVLETVAPVAPVSCVPSALSGTVLRCQDKGPNAPERYT 167
Qy 173 WYRNDVPLPTDSRANPRFRNSSHNLSEGTGLVFAVHKDSCGYCTASNDAGSARCEE 232
Db 168 WFKDGRILLENPRLSQSTNSSYMNTKTGTLQFNVTSSKLDGTGEYSCEARNVSVGRCPG 227
Qy 233 OMEVYDINIGTIGGVLVVALITLITGICAYRGYF 272
Db 228 KRMQVDDINISGIIAAVVVALVSVCGLGVCYARQKGYF 267

RESULT 9
US-09-254-465A-10
Sequence 10, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
FILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1 (US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 10
LENGTH: 300

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/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 64
/ LENGTH: 312
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match      27.9% Score 456.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 1.2e-38;
Matches 104; Conservative 51; Mismatches 104; Indels 21; Gaps 7;
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QY 1 MALRRPRLRLCARLPDFFLLFRGCLIG----AVNLKSNRTPVYQ--EFESVELSC 53
DB 1 MAARRRHRL-----LTLRLRYLVVALGYHKAYGFSAPDQOVTAVEYDEALLAC 50

QY 54 IITDSQSDPRIEMKKIQDQTTVFPDNKIQDLAGRAEILGKTSKIMVWTRDSALY 113
DB 51 -KTPFKKTVSRLEWKL-GRSVGFVYIQQLQDLPKRAEMT-DENIRIKNVTNRSDAGKI 107

QY 114 RCEVYANDR-KEIDELIVELTVQVKEVTEVCRAVPKAVPVGNATLHCDSGPHRPHYS 172
DB 108 RCEVASBSEQONLEBDTVLLEVAVAPVSCVPSALSGLTVELRCQDKGNPAPEXT 167

QY 173 WYRNDVLPFDSDRANPFRNSSSHLNETGTIVFTAHKDSQCYCIASNDGSRCEE 232
DB 168 WPKDGIILNPNRIGSOSTSSYTMNKTSTLPNTVSKLDTSEYSCAANSVGVRCCG 227

QY 233 QMEVYDNLIGIGLVVLAVALATLTIGICCAVRRGYF 272
DB 228 KRMQVDDLNTSGIIAAVVVALVISVGLGVCAQRKGYF 267

RESULT 7
US-09-905-125A-64
Sequence 64, Application US/09050125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Askenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen

```
/ APPLICANT: Fong, Sherman  
/ APPLICANT: Gao, Wei-Qiang  
/ APPLICANT: Gerber, Hanspeter  
/ APPLICANT: Gerltsen, Mary E.  
/ APPLICANT: Goddard, A.  
/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, Christopher J.  
/ APPLICANT: Gurney, Austin L.  
/ APPLICANT: Hillan, Kenneth J.  
/ APPLICANT: Kljavin, Ivar J.  
/ APPLICANT: Mather, Jennie P.  
/ APPLICANT: Pan, James  
/ APPLICANT: Paoni, Nicholas F.  
/ APPLICANT: Roy, Margaret Ann  
/ APPLICANT: Stewart, Timothy A.  
/ APPLICANT: Tumas, Daniel  
/ APPLICANT: Williams, P. Mickey  
/ APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-12  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US/09/905,125A  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 64  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-905-125A-64

Query Match      27.9% Score 456.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 1.2e-38;
Matches 104; Conservative 51; Mismatches 104; Indels 21; Gaps 7;
```

QY 1 MALRRPRLRLCARLPDFFLLFRGCLIG----AVNLKSNRTPVYQ--EFESVELSC 53
DB 1 MAARRRHRL-----LTLRLRYLVVALGYHKAYGFSAPDQOVTAVEYDEALLAC 50

QY 54 IITDSQSDPRIEMKKIQDQTTVFPDNKIQDLAGRAEILGKTSKIMVWTRDSALY 113

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 76
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (58)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

Query Match 29.1%; Score 476; DB 4; Length 298;
Best Local Similarity 35.8%; Pred. No. 1,1e-40;

Matches 114; Conservative 59; Mismatches 117; Indels 28; Gaps 10;

QY 1 MALRRPRLRLCARLPDFFLLFRGLIG-----AVNKKSNRPVVO--EFESVELSC 53
DB 1 MARRRHRL-----LILLRLVVALGYHKAVGSAPRDQVVAVYQEAIALC 50
QY 54 IITDSQTSDRIRWKIODEQTTVFEDNKIOGDLGRAELIKTSLKTMNTRDSALY 113
DB 51 -KTPKKTIVSRLEWKI-GRSVFVYQOTLQDFNRAEMI-DEFIRIKNVTSDAGKY 107
QY 114 RCEVVAANDR-KEIDEIVIELTVQVCPVPCVPRKAVPVGKXATLHCQESGHPPHYS 172
DB 108 RCEVSAPEQGNLEEDTVLEVLVAPVSCVPSALSGTVELRCQDKGNPAPEYT 167
QY 173 WYRNDVLPDPSRANPRFNSSSHLNSETGLVFTAVHKDQSGQYCIASNDGSRCEE 232
DB 168 WFKDGIILLENPRLGOSSTSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNVGYRCPG 227
QY 233 QMEVVDNLNGIIGLVVLAVALTLTGICAYRGYFINNKQDGESYKNGKPDGVN 292
DB 228 KRMQVDNLISGIIAAVVAVALVISGGLGVCAQRKGY--SKE--TSQ--KSNSS 280
QY 293 YIRDEGDTRHKSSEYI 310
DB 281 KATMSNDPRHTKSFII 298

RESULT 5

US-09-254-465A-9

Sequence 9, Application US/09254465A

Patent No. 6410708

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Nadler, Mary A.

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

FILE REFERENCE: P1216R1(US)

CURRENT APPLICATION NUMBER: US/09/254,465A

PRIOR FILING DATE: 1999-03-05

PRIOR APPLICATION NUMBER: PCT/US98/24855

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: US 60/066,364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 60/078,936

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: PCT/US98/19437

PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 9
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-9

Query Match 27.9%; Score 456.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 1,2e-38;
Matches 104; Conservative 51; Mismatches 104; Indels 21; Gaps 7;

QY 1 MALRRPRLRLCARLPDFFLLFRGLIG-----AVNKKSNRPVVO--EFESVELSC 53
DB 1 MARRRHRL-----LILLRLVVALGYHKAVGSAPRDQVVAVYQEAIALC 50
QY 54 IITDSQTSDRIRWKIODEQTTVFEDNKIOGDLGRAELIKTSLKTMNTRDSALY 113
DB 51 -KTPKKTIVSRLEWKI-GRSVFVYQOTLQDFNRAEMI-DEFIRIKNVTSDAGKY 107
QY 114 RCEVVAANDR-KEIDEIVIELTVQVCPVPCVPRKAVPVGKXATLHCQESGHPPHYS 172
DB 108 RCEVSAPEQGNLEEDTVLEVLVAPVSCVPSALSGTVELRCQDKGNPAPEYT 167
QY 173 WYRNDVLPDPSRANPRFNSSSHLNSETGLVFTAVHKDQSGQYCIASNDGSRCEE 232
DB 168 WFKDGIILLENPRLGOSSTSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNVGYRCPG 227
QY 233 QMEVVDNLNGIIGLVVLAVALTLTGICAYRGYFINNKQDGESYKNGKPDGVN 292
DB 228 KRMQVDNLISGIIAAVVAVALVISGGLGVCAQRKGYF 267

RESULT 6

US-09-907-794A-4

Sequence 64, Application US/0907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Grimaldi, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavira, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

PRIOR FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

QY 181 PTDSRANPRFRNSSHINSETGLVFTAVHKDSDGQYCYCLASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFRNSSHINSETGLVFTAVHKDSDGQYCYCLASNDAGSARCEQMEVYDL 240
QY 241 NIGGIIGVVLVAVLALITLIGICAYRGGYFINNKDGSYKPGKPDGVNVRTDEEG 300
DB 241 NIGGIIGVVLVAVLALITLIGICAYRGGYFINNKDGSYKPGKPDGVNVRTDEEG 300
QY 301 DFRKXSFVI 310
DB 301 DFRKXSFVI 310

RESULT 3
US-09-902-775A-423
Sequence 423, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30939
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-423

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 2.8e-159;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLLRGLLIGAVNKKSNRTPVVOEFSEVLSCTITTSQT 60
DB 1 MALRRPRLRLCARLPDFLLLRGLLIGAVNKKSNRTPVVOEFSEVLSCTITTSQT 60
QY 61 SDPRIEWKTIODEQTVVFPDNKIQGLAGRAEILGKTSKINWTRDSALYCEVVAR 120
DB 61 SDPRIEWKTIODEQTVVFPDNKIQGLAGRAEILGKTSKINWTRDSALYCEVVAR 120
QY 121 NDRKEIDIEVIELVQKPYTPVCRVPKAVPGVGMATLHCQESGHRPHYSWYRNVPL 180
DB 121 NDRKEIDIEVIELVQKPYTPVCRVPKAVPGVGMATLHCQESGHRPHYSWYRNVPL 180
QY 181 PTDSRANPRFRNSSHINSETGLVFTAVHKDSDGQYCYCLASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFRNSSHINSETGLVFTAVHKDSDGQYCYCLASNDAGSARCEQMEVYDL 240
QY 241 NIGGIIGVVLVAVLALITLIGICAYRGGYFINNKDGSYKPGKPDGVNVRTDEEG 300
DB 241 NIGGIIGVVLVAVLALITLIGICAYRGGYFINNKDGSYKPGKPDGVNVRTDEEG 300
QY 301 DFRKXSFVI 310
DB 301 DFRKXSFVI 310

RESULT 4
US-09-152-060-76
Sequence 76, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 2,8e-159;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAARRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTPVVQEFSEVLSCTITDSQT 60
DB 1 MAARRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTPVVQEFSEVLSCTITDSQT 60
QY 61 SDPRIEMKKIODEQTTVFEPDNKIQDLAGRAELIKTSIKIMVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIODEQTTVFEPDNKIQDLAGRAELIKTSIKIMVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQYKPTVPCRVKAVPVGMATLHCQESGHRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQYKPTVPCRVKAVPVGMATLHCQESGHRPHYSWYRNDVPL 180
QY 181 PTPSRANPRFRNSSSHNSSTGLVFTAVKDSGQYCIASNDAGSACEQEMEYVDL 240
DB 181 PTPSRANPRFRNSSSHNSSTGLVFTAVKDSGQYCIASNDAGSACEQEMEYVDL 240
QY 241 NIGGIIGVVLVAVLALITLIGICCAVRGYPFNNKQDGSYNNPKGPDGVNVRTDEBG 300
DB 241 NIGGIIGVVLVAVLALITLIGICCAVRGYPFNNKQDGSYNNPKGPDGVNVRTDEBG 300
QY 301 DFRKXSFVI 310
DB 301 DFRKXSFVI 310

RESULT 2
US-09-905-125A-423
Sequence 423, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashtkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deancysers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 2,8e-159;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAARRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTPVVQEFSEVLSCTITDSQT 60
DB 1 MAARRPRLRLCARLPDFLLFRGCLIGAVNLKSNRTPVVQEFSEVLSCTITDSQT 60
QY 61 SDPRIEMKKIODEQTTVFEPDNKIQDLAGRAELIKTSIKIMVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIODEQTTVFEPDNKIQDLAGRAELIKTSIKIMVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQYKPTVPCRVKAVPVGMATLHCQESGHRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQYKPTVPCRVKAVPVGMATLHCQESGHRPHYSWYRNDVPL 180

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-125A-423

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:14:48 ; Search time 22 Seconds
(without alignments)
727.457 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLCARLPDFL.....VNYITDEGDPHKMSFVI 310

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

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4	475	29.1	298	4	US-09-152-060-76
5	456.5	27.9	312	4	US-09-254-465A-9
6	456.5	27.9	312	4	US-09-907-794A-64
7	456.5	27.9	312	4	US-09-905-125A-64
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9	449.5	27.5	300	4	US-09-254-465A-10
10	419	25.6	299	3	US-09-188-930-331
11	419	25.6	299	4	US-09-462-370-2
12	419	25.6	299	4	US-09-254-465A-1
13	419	25.6	299	4	US-09-312-283C-189
14	419	25.6	299	4	US-09-312-283C-331
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16	419	25.6	299	4	US-09-905-125A-119
17	419	25.6	299	4	US-09-902-775A-119
18	407	24.9	299	3	US-09-188-930-189
19	387.5	23.7	260	4	US-09-254-465A-23
20	387.5	23.7	263	4	US-09-254-465A-25
21	283	17.3	305	4	US-09-462-370-4
22	231.5	14.2	319	1	US-08-597-495B-22
23	231.5	14.2	319	3	US-09-068-051A-22
24	231.5	14.2	319	4	US-09-336-536-67
25	231.5	14.2	319	4	US-09-254-465A-6
26	230.5	13.5	270	4	US-09-254-465A-24
27	220.5	13.5	273	4	US-09-254-465A-26

28	215.5	13.2	318	3	US-09-068-051A-32	Sequence 32, Appl
29	198.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appl
30	175.5	10.7	370	4	US-09-336-536-28	Sequence 28, Appl
31	171.5	10.5	390	2	US-08-979-424-1	Sequence 1, Appl
32	171.5	10.5	390	4	US-09-907-794A-39	Sequence 39, Appl
33	171.5	10.5	390	4	US-09-905-125A-39	Sequence 39, Appl
34	171.5	10.5	390	4	US-09-902-775A-39	Sequence 39, Appl
35	171.5	10.5	394	4	US-09-336-536-39	Sequence 39, Appl
36	168.5	10.3	344	4	US-09-336-536-29	Sequence 29, Appl
37	168.5	10.3	398	4	US-09-778-510-6	Sequence 6, Appl
38	168.5	10.3	398	4	US-09-907-794A-84	Sequence 84, Appl
39	168.5	10.3	398	4	US-09-905-125A-84	Sequence 84, Appl
40	168.5	10.3	398	4	US-09-902-775A-84	Sequence 84, Appl
41	167	10.2	365	4	US-09-336-536-40	Sequence 40, Appl
42	164.5	10.1	345	4	US-09-336-536-31	Sequence 31, Appl
43	164.5	10.1	365	3	US-08-928-383B-2	Sequence 2, Appl
44	161.5	9.9	365	2	US-08-979-424-3	Sequence 3, Appl
45	161.5	9.9	365	3	US-09-272-496-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-907-794A-423
Sequence 423, Application US/0907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan J.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerstein, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
PRIORITY FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

ALIGNMENTS

RESULT 1
US-09-907-794A-423
Sequence 423, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
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DB 1 MALRRPRLRCARLPDFELLFRGCLIGAVNKKSNRTVPVOEFSVELSCITTSQT 60
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DB 61 SDPRIEMWKIQDEQTYVFPDNKIQGLAGRAEILGKTSLKIMVTRDSALYCEVVAR 120
QY 121 NDRKIDIVIELTQVQVPTVPCGVPKAVPVGKATLHCESGHPREHSWYRNDVPL 180
DB 121 NDRKIDIVIELTQVQVPTVPCGVPKAVPVGKATLHCESGHPREHSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFRNSSSHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQMEVYDL 240
QY 241 NIGGIIIGVLYLVATLITIGICAYRGYFINNKDGESYKPKGKDDGYNTIRTDSEG 300
DB 241 NIGGIIIGVLYLVATLITIGICAYRGYFINNKDGESYKPKGKDDGYNTIRTDSEG 300
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RESULT 2
US-09-905-125A-423
Sequence 423, Application US/09905125A
Patent No. 6654376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414

Mon Apr 12 09:42:26 2004

us-09-831-805a-6.oligo.rat

Page 1

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:22:09 ; Search time 22 Seconds
(without alignment)

727.457 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 310

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Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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90 209 67.4 310 14 US-10-033-435-20 Sequence 20, Appl
91 209 67.4 310 14 US-10-176-746-538 Sequence 538, App
92 209 67.4 310 14 US-10-176-921-538 Sequence 538, App
93 209 67.4 310 14 US-10-032-990-20 Sequence 20, Appl
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ALIGNMENTS

RESULT 1
US-09-909-320-423
Sequence 423, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvarcoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,658
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-423
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Best Local Similarity 99.7%; Pred. No. 9.1e-195;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 SDPRLEWKKIQDEQTYVFFDNKIQSLAGRAELIGKTSKIMVTRDSALRYCEVVAR 120
QY 121 NDRKEIDIVELVQVKPTPVCRVPRKAVPVGMATLHCQESGHRPHYSWRNVPL 180
DB 121 NDRKEIDIVELVQVKPTPVCRVPRKAVPVGMATLHCQESGHRPHYSWRNVPL 180
QY 181 PTDSRANPRFNSSSHNSEITGLVFTAVHNDGQYVCIASNDAGARCEQMEVYDL 240
DB 181 PTDSRANPRFNSSSHNSEITGLVFTAVHNDGQYVCIASNDAGARCEQMEVYDL 240
QY 241 NIGGITGVVVLVLAITLTGICAYRGGYFINNKDGSYKNGKPDGNTYRTSEG 300
DB 241 NIGGITGVVVLVLAITLTGICAYRGGYFINNKDGSYKNGKPDGNTYRTSEG 300
QY 301 DFRHKSFFVI 310
DB 301 DFRHKSFFVI 310
RESULT 2
US-09-909-088B-423
Sequence 423, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvarcoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James

Mon Apr 12 09:42:26 2004

us-09-831-805a-6.oligo.rapb

Page 1

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:24:55 ; Search time 46 Seconds
(without alignments)
1771.973 Million cell updates/sec

Title: US-09-831-805a-6

Perfect score: 310

Sequence: 1 MLRRPRRLCARLPDFL.....VYIRTDEGDFRHSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications_AA.*

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11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	209	67.4	310	9 US-09-902-853-423	Sequence 423, App
5	209	67.4	310	9 US-09-907-824-423	Sequence 423, App
6	209	67.4	310	9 US-09-907-841-423	Sequence 423, App
7	209	67.4	310	10 US-09-904-011-423	Sequence 423, App
8	209	67.4	310	10 US-09-906-742-423	Sequence 423, App
9	209	67.4	310	10 US-09-906-838-423	Sequence 423, App
10	209	67.4	310	10 US-09-907-613-423	Sequence 423, App
11	209	67.4	310	10 US-09-907-942-423	Sequence 423, App
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70	209	67.4	310	11 US-09-833-245-2047	Sequence 2047, App
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85	209	67.4	310	13 US-10-033-244-423	Sequence 423, App
86	209	67.4	310	14 US-10-028-072-538	Sequence 538, App
87	209	67.4	310	14 US-10-121-049-538	Sequence 538, App
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99 209 67.4 310 7 ADB18435 Adb18435 Human PRO
100 209 67.4 310 7 ADA87118 Ada87118 Novel hum

ALIGNMENTS

RESULT 1

AA96294

ID AAY96294 standard; protein; 310 AA.

AC AAY96294;

DT 16-AUG-2000 (first entry)

DE Human IGFAM-6 immunoglobulin.

XX Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;

KM infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..30 /label= signal_peptide

FT Protein 31..310 /label= IGFAM-6

FT Domain 46..117 /label= Ig_domain

FT Domain 153..221 /label= Ig_domain

FT Domain 238..260 /label= transmembrane_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

XX Lu DM, Lai P, Hillman UL, Yang U;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27386.

XX Claim 1; Page 82-83; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein

XX IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is

XX expressed in reproductive, nervous and cardiovascular tissue, where

XX cancer and inflammation are common. The gene, protein, its antibodies,

XX agonists and antagonists are suitable for diagnosing and treating many

XX diseases, including cancer, immune system disorders (such as

XX inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,

XX athyrosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,

XX empty-soma, Graves' disease, hepatitis, multiple sclerosis, psoriasis,

XX rheumatoid arthritis, scleroderma, systemic lupus erythematosus and

XX ulcerative colitis), complications of cancer, haemodialysis and

XX extracorporeal circulation, trauma and haematopoietic cancer (such as

XX leukaemia) and infections caused by bacteria, viruses, fungi or parasites

XX Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 4,3e-296;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SDPRLEWKKIODEQTYTFPNKIQGLAGRAELIGKTSIKINWTRDSALYRCEVAR 120
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DB 121 NDRKEIDIEIVELYQVQVTPVCRVPKAVPVGMATLHCQESGHRPHYSKTRNDVPL 180
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DB 181 PTDSPANRFRNSSSHLNSEGTIVFTAVHKDPSGOYYCIAINDAGSARCEQMEVYDL 240
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DB 241 NIGGIIGVVLVAVLALITLIGICAVRGGYFINNKODGESYKPKGPDGVNVI RTDDEG 300
QY 301 DFRKSSFYI 310
DB 301 DFRKSSFYI 310

RESULT 2

AA96735

ID AAY96735 standard; protein; 310 AA.

XX AAY96735;

XX 26-SEP-2000 (first entry)

XX PRO1868, an A33 antigen homologue.

XX PRO1868, A33 antigen, secreted protein; transmembrane protein;

XX anti-inflammatory; cytostatic; recombinant production; gene therapy.

XX Homo sapiens.

XX FH Key

FT Peptide 1..30 /label= signal_peptide

FT Modified-site 26..31 /note= "N-myristoylation site"

FT Modified-site 69..77 /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 104..107 /note= "N-glycosylation site"

FT Modified-site 106..109 /note= "Casein kinase II phosphorylation site"

FT Modified-site 107..110 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 192..195 /note= "N-glycosylation site"

FT Modified-site 215..220 /note= "N-myristoylation site"

FT Modified-site 226..231 /note= "N-myristoylation site"

FT Domain 243..263 /label= "Transmembrane_domain"

FT Modified-site 243..248 /note= "N-myristoylation site"

FT Modified-site 244..249 /note= "N-myristoylation site"

FT Modified-site 262..267 /note= "N-myristoylation site"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:16:49 ; Search time 60 Seconds
(without alignments)

1459.829 Million cell updates/sec

Title: us-09-831-805A-6

Perfect score: 310
Sequence: 1 MAURRPPRLRCALPDFFL.....VNYRTDEGDFRHKSSFYI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: A_Geneseg 29Jan04:*

1: genesegp1980s:*
2: genesegp1990s:*
3: genesegp2000s:*
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5: genesegp2002s:*
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8: genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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27	209	67.4	310	6	ADA57309 Human sec
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82	209	67.4	310	6	ABP71277 Human jun
83	209	67.4	310	6	ABP71277 Human jun
84	209	67.4	310	6	ABP71277 Human jun
85	209	67.4	310	6	ABP71277 Human jun
86	209	67.4	310	6	ABP71277 Human jun
87	209	67.4	310	6	ABP71277 Human jun
88	209	67.4	310	6	ABP71277 Human jun
89	209	67.4	310	6	ABP71277 Human jun
90	209	67.4	310	6	ABP71277 Human jun
91	209	67.4	310	6	ABP71277 Human jun
92	209	67.4	310	6	ABP71277 Human jun
93	209	67.4	310	6	ABP71277 Human jun
94	209	67.4	310	6	ABP71277 Human jun
95	209	67.4	310	6	ABP71277 Human jun
96	209	67.4	310	6	ABP71277 Human jun
97	209	67.4	310	6	ABP71277 Human jun
98	209	67.4	310	7	ADA77655 Human PRO

90 2.3 210 16 Q8DSW6 Q8dsw6 streptococc
91 7 2.3 211 16 Q9CDV2 Q9cdv2 lactococcus
92 7 2.3 214 2 O32618 O32618 helicobacte
93 7 2.3 214 6 O62722 O62722 cryoclaigus
94 7 2.3 215 16 Q837X2 Q837x2 enterococc
95 7 2.3 217 12 Q9YMN1 Q9ymn1 lymantria d
96 7 2.3 219 16 Q8KDL2 Q8kdl2 chirobium
97 7 2.3 221 11 Q8C8M1 Q8c8m1 mus musculu
98 7 2.3 224 11 Q9R1M6 Q9r1m6 mus musculu
99 7 2.3 227 12 Q91BE2 Q91be2 spodoptera
100 7 2.3 229 16 Q8FR05 Q8fr05 corynebacte

ALIGNMENTS

RESULT 1

Q9BX67 PRELIMINARY; PRT; 310 AA.

AC Q9BX67; PRELIMINARY; PRT; 310 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurand-Jones M.A., Johnson-Jeger C., Wong C., Dupasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurand-Jones M.A., Johnson-Jeger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial junctions."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Isogai T., Oka T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K., Masuno Y., Oho T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NBD human CDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AAC7221.1; -
DR EMBL; AJ344431; CAC69845.1; -
DR EMBL; AF448478; AAM20925.1; -
DR EMBL; AK074769; BAC1195.1; -
DR EMBL; AK075309; BAC11538.1; -
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS50835; IG_LIKE; 2.

KW Hypothetical protein; Signal.
FT SIGNAL
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF3EADAB9 CRC64;
Query Match 67.4%; Score 209; DB 4; Length 310;
Best local similarity 99.7%; Pred. No. 3.2e-214;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLILFRGCLIGAVNLKSSNRTPVVQEFSEVSLCITTSQT 60
DB 1 MALRRPRLRLCARLPDFLLILFRGCLIGAVNLKSSNRTPVVQEFSEVSLCITTSQT 60
QY 61 SDPRLEWKIODEQTYVFPENKIQGLDAGRAELIGKTSIKIMVTRDSALRCEVVAR 120
DB 61 SDPRLEWKIODEQTYVFPENKIQGLDAGRAELIGKTSIKIMVTRDSALRCEVVAR 120
QY 121 NDRKEIDELIVETLVQKVPYTPVCRVPEKAVPVGKATLHCQSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDELIVETLVQKVPYTPVCRVPEKAVPVGKATLHCQSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANRFRNSSSHLNSERTGLVFTAVKDDSGQYYCIASNDAGARCECEMEYDYL 240
DB 181 PTDSRANRFRNSSSHLNSERTGLVFTAVKDDSGQYYCIASNDAGARCECEMEYDYL 240
QY 241 NIGGIIGVVLVAVLALITIGICCAVRRGYFINNKDGSYKPKGKPDGVNVRTDSEG 300
DB 241 NIGGIIGVVLVAVLALITIGICCAVRRGYFINNKDGSYKPKGKPDGVNVRTDSEG 300
QY 301 DFRKKSFEVI 310
DB 301 DFRKKSFEVI 310

RESULT 2

Q8WVL8 PRELIMINARY; PRT; 355 AA.
AC Q8WVL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hearn T.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within 11q24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during cardiogenesis."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig_2.
DR SMART; SMO0408; IGC2_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR Immunoglobulin domain.
KM CHAIN 76
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7BD4F8 CQC64;
Query Match 67.4%; Score 209; DB 4; Length 355;
Best local similarity 99.7%; Pred. No. 3.7e-214;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFLLILFRGCLIGAVNLKSSNRTPVVQEFSEVSLCITTSQT 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:20:39 ; Search time 46 Seconds

(without alignment)
2126.318 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFPL.....VNYRTDESGDPKXSVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 31518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	67.4	310	4 Q9BX57	Q9BX57 homo sapien
2	209	67.4	355	4 Q8WML8	Q8WML8 homo sapien
3	134	43.2	309	4 Q96FL1	Q96FL1 homo sapien
4	32	10.3	310	11 Q9DB87	Q9DB87 mus musculi
5	28	9.0	310	11 Q9DIM9	Q9DIM9 mus musculi
6	28	9.0	310	11 Q9EPK4	Q9EPK4 mus musculi
7	13	4.2	64	11 Q8RT59	Q8RT59 mus musculi
8	8	2.6	39	7 Q9TNT2	Q9TNT2 homo sapien
9	8	2.6	67	7 Q8HWG1	Q8HWG1 homo sapien
10	8	2.6	76	5 Q867W1	Q867W1 procambius
11	8	2.6	131	5 Q818S1	Q818S1 anopheles g
12	8	2.6	154	11 Q8C4V2	Q8C4V2 mus musculi
13	8	2.6	231	16 Q89E35	Q89E35 bradyrhizob
14	8	2.6	231	17 Q87QT5	Q87QT5 methanobact
15	8	2.6	232	17 Q8ZSR8	Q8ZSR8 pyrobaculum
16	8	2.6	233	10 Q9LR49	Q9LR49 arabidopsis

17	246	5	Q96EC0	Q96EC0 caenorhabdi
18	294	16	Q98E09	Q98E09 rhizobium l
19	309	5	Q9N4Y9	Q9N4Y9 caenorhabdi
20	322	2	Q9RP17	Q9RP17 desulfotoba
21	336	10	Q9C7E9	Q9C7E9 arabidopsis
22	338	7	Q9MXL5	Q9MXL5 pan troglod
23	348	7	Q9MW19	Q9MW19 gorilla gor
24	348	16	Q9PR46	Q9PR46 ureaplasma
25	363	7	Q9SHC2	Q9SHC2 homo sapien
26	363	7	Q9XRX8	Q9XRX8 pongo pygma
27	365	7	Q9XRX7	Q9XRX7 pongo pygma
28	365	7	Q9MXG4	Q9MXG4 pan troglod
29	366	6	Q46684	Q46684 pan troglod
30	366	7	Q8MH10	Q8MH10 pongo pygma
31	366	7	Q8MH11	Q8MH11 pongo pygma
32	366	7	Q8MHG8	Q8MHG8 pongo pygma
33	366	7	Q8MHG9	Q8MHG9 pongo pygma
34	366	7	Q19617	Q19617 homo sapien
35	366	7	Q860B0	Q860B0 homo sapien
36	366	7	Q85ZX8	Q85ZX8 homo sapien
37	366	7	Q9TPU2	Q9TPU2 pan troglod
38	366	7	Q9MXD2	Q9MXD2 pan troglod
39	366	7	Q7YQZ2	Q7YQZ2 homo sapien
40	449	16	Q8CWZ7	Q8CWZ7 streptococc
41	452	16	Q8GSD2	Q8GSD2 bifidobacte
42	492	16	Q8ZIU9	Q8ZIU9 salmonella
43	659	16	Q8EK37	Q8EK37 shewanella
44	784	16	Q9CTF4	Q9CTF4 lactococcus
45	1290	13	Q9KCE1	Q9KCE1 gallus gall
46	67	4	Q8N1B5	Q8N1B5 homo sapien
47	82	16	Q837K2	Q837K2 enterococcu
48	85	12	Q99GX8	Q99GX8 helicoverpa
49	86	16	Q8ERD1	Q8ERD1 oceanobacill
50	92	10	Q8LFP4	Q8LFP4 arabidopsis
51	92	10	Q8GX99	Q8GX99 arabidopsis
52	100	10	Q84QM7	Q84QM7 cryza sativ
53	104	9	Q8W6S1	Q8W6S1 bacterioph
54	112	16	Q8CSN1	Q8CSN1 staphylococ
55	113	16	Q928J9	Q928J9 listeria in
56	116	17	Q8U3Z7	Q8U3Z7 pyrococcus
57	135	2	Q8RTU0	Q8RTU0 streptococc
58	144	10	Q8LNO1	Q8LNO1 cryza sativ
59	144	17	Q81KY1	Q81KY1 bacillus an
60	146	17	Q973F7	Q973F7 sulfolobus
61	148	16	Q821I9	Q821I9 streptomyc
62	149	6	Q7YS63	Q7YS63 sus scrofa
63	155	16	Q88B00	Q88B00 pseudomonas
64	158	2	Q8EWM3	Q8EWM3 streptomyc
65	158	16	Q8XSX1	Q8XSX1 ralsotonia s
66	163	9	Q7YS14	Q7YS14 bacterioph
67	163	2	Q8GD28	Q8GD28 bordetella
68	168	16	Q897U4	Q897U4 clostridium
69	171	16	Q06422	Q06422 mycobacteri
70	171	16	Q7UIS3	Q7UIS3 mycobacteri
71	172	10	Q9SZQ8	Q9SZQ8 arabidopsis
72	173	5	Q22966	Q22966 caenorhabdi
73	173	10	Q64567	Q64567 arabidopsis
74	173	17	Q97ZK3	Q97ZK3 sulfolobus
75	177	16	Q931Y0	Q931Y0 staphylococ
76	177	16	Q8X7L2	Q8X7L2 escherichia
77	179	16	Q9KRC2	Q9KRC2 streptomyc
78	189	17	Q8TWY8	Q8TWY8 methanobact
79	191	10	Q9XHM2	Q9XHM2 medicago tr
80	194	16	Q8EZ34	Q8EZ34 leptospira
81	200	10	Q8YV74	Q8YV74 arabidopsis
82	201	16	Q83N81	Q83N81 tropheryma
83	201	16	Q83F16	Q83F16 tropheryma
84	202	6	Q9TUF4	Q9TUF4 propithecus
85	202	6	Q9TUF5	Q9TUF5 cercopithec
86	204	2	Q8KU14	Q8KU14 actinosyne
87	208	10	Q80501	Q80501 arabidopsis
88	208	10	Q40525	Q40525 nicotiana t
89	208	10	Q8H4Q9	Q8H4Q9 cryza sativ

TX3A_PHONI STANDARD; PRT; 80 AA.

AC P81793;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotoxin Pn3 precursor
 OS Phosphatidylcholine transferase (Bacterial armed spider)
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 CC Araneomorphae; Entelegynae; Lycosidae; Ctenidae; Phlebotominae;
 CC NCBI_TaxID=6918;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=9035416; PubMed=9839681;
 RA Kalapothakis E., Penatier C.L., Leao R.M., Cruz J.S., Prado V.F.,
 RA Cordeiro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,
 RA Gomez M.V., Beltrao P.S.L.;
 RT "Cloning, cDNA sequence analysis and patch clamp studies of a toxin
 RT from the venom of the armed spider (Phlebotominae nigriventris).";
 RT Toxicon 36:1971-1980(1998)
 CC -1- FUNCTION: Antagonist of L-type calcium channels (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the spider toxin Tx3 family.
 DR InterPro: IPR004169; SpiderToxin.
 DR Pfam: PF02819; SpiderToxin; 1.
 KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
 KM Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 37 BY SIMILARITY.
 FT CHAIN 38 71 NEUROTOXIN Pn3.
 FT PROPEP 72 80 BY SIMILARITY.
 SQ SEQUENCE 80 AA; 8937 MW; B5BF209257EB6793 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 256 LATITLGI 263
 DB 12 LATITLGI 19

RESULT 2
 ID 1C02 GORGO STANDARD; PRT; 366 AA.
 AC P30385;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Class I histocompatibility antigen, GOGO-CO201 alpha chain precursor.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
 CC NCBI_TaxID=9595;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9207860; PubMed=1744581;
 RA Lawlor D.A., Warren E., Taylor P., Parham P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 RT to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
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 or send an email to license@ib-sib.ch).

CC EMBL: X60251; CAA42803.1; .
 CC PIR: J0545; J0545.
 CC HSSP: P30685; 1A9E.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR001039; MHC_1.
 DR Pfam: PF00047; IG_1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IG1; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; FALSE NEG.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 366
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 333
 FT DOMAIN 334 366
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 SQ SEQUENCE 366 AA; 40954 MW; 05E159364C76F6C5 CRC64; (BY SIMILARITY).

Query Match 2.6%; Score 8; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VLVVLAVL 256
 DB 317 VLVVLAVL 324

RESULT 3
 ID 1C03 GORGO STANDARD; PRT; 366 AA.
 AC P30386;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Class I histocompatibility antigen, GOGO-CO202 alpha chain precursor.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
 CC NCBI_TaxID=9595;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9207860; PubMed=1744581;
 RA Lawlor D.A., Warren E., Taylor P., Parham P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 RT to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:20:04 ; Search time 18 Seconds

(without alignments)
896.764 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MAURRPPRLRLCARLPDFL.....VNIYRDEGDRHAKSSFVI.310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	80	1	TX3A_PHOXI
2	8	2.6	366	1	IC02_GORGO
3	8	2.6	366	1	IC03_GORGO
4	8	2.6	366	1	IC04_GORGO
5	8	2.6	366	1	IC07_HUMAN
6	8	2.6	366	1	IC18_HUMAN
7	8	2.6	435	1	YGIK_SALTY
8	7	2.3	161	1	TATB_STRCO
9	7	2.3	224	1	XIRL_MOUSE
10	7	2.3	242	1	RS2_SHEON
11	7	2.3	244	1	TNFC_HUMAN
12	7	2.3	244	1	TNFC_PANTR
13	7	2.3	302	1	HTPX_AQUAE
14	7	2.3	306	1	TNFC_MOUSE
15	7	2.3	310	1	TNFC_MARMO
16	7	2.3	333	1	GPR8_HUMAN
17	7	2.3	343	1	HMD_METYO
18	7	2.3	374	1	TRML_SULFO
19	7	2.3	403	1	TYRP_ECOLI
20	7	2.3	417	1	PVR_CERAE
21	7	2.3	417	1	PVR_HUMAN
22	7	2.3	418	1	SYTF_MOUSE
23	7	2.3	454	1	APV_SOLTU
24	7	2.3	481	1	LMRA_STRLN
25	7	2.3	491	1	CPB4_RABIT
26	7	2.3	491	1	CPB5_RABIT
27	7	2.3	524	1	IRL2_HUMAN
28	7	2.3	574	1	IRL2_MOUSE
29	7	2.3	595	1	IFP2_ARCFU
30	7	2.3	617	1	PYS1_PSEAE
31	7	2.3	643	1	S212_HUMAN
32	7	2.3	643	1	S212_MOUSE
33	7	2.3	643	1	S212_RAT

34	7	2.3	688	1	PYS2_PSEAE
35	7	2.3	693	1	NCPR_ASPNG
36	7	2.3	697	1	TM22_CHICK
37	7	2.3	721	1	YIYI_ECOLI
38	7	2.3	729	1	GOA5_MOUSE
39	7	2.3	758	1	SC18_YEAST
40	7	2.3	840	1	CC16_YEAST
41	7	2.3	909	1	RRS2_ARATH
42	7	2.3	981	1	SCA4_RICCE
43	7	2.3	987	1	K6P1_CANAL
44	7	2.3	991	1	SCA4_RICCI
45	7	2.3	1011	1	SCA4_RICCI
46	7	2.3	1011	1	SCA4_RICCN
47	7	2.3	1012	1	SCA4_RICCL
48	7	2.3	1013	1	SCA4_RICRH
49	7	2.3	1018	1	SCA4_RICCN
50	7	2.3	1022	1	SCA4_RICCN
51	7	2.3	1053	1	ITR3_MOUSE
52	7	2.3	1066	1	ITR3_CRISP
53	7	2.3	1066	1	ITR3_HUMAN
54	7	2.3	1105	1	YRGE_ECOLI
55	7	2.3	1126	1	HPS5_MOUSE
56	7	2.3	1142	1	PAK1_YEAST
57	7	2.3	1169	1	EXSB_BOREU
58	7	2.3	1234	1	YMX5_CABEL
59	7	2.3	4684	1	PLE1_HUMAN
60	7	2.3	5065	1	EPPL_HUMAN
61	7	1.9	38	1	CRS3_NOTCO
62	7	1.9	46	1	LHAI_ECTHA
63	7	1.9	57	1	ANDP_DROMA
64	7	1.9	57	1	ANDP_DROME
65	7	1.9	57	1	ANDP_DROSE
66	7	1.9	57	1	Y160_ARCFU
67	7	1.9	60	1	ANDP_DROSI
68	7	1.9	61	1	RS14_MYCCA
69	7	1.9	64	1	YD16_SCHPO
70	7	1.9	69	1	BRIP_RANPI
71	7	1.9	74	1	SRP_SOYAN
72	7	1.9	76	1	SECG_BACSU
73	7	1.9	82	1	TX32_PHOXI
74	7	1.9	83	1	TX31_PHOXI
75	7	1.9	86	1	PTHP_STRNU
76	7	1.9	87	1	PTHP_BACID
77	7	1.9	87	1	PTHP_STRBO
78	7	1.9	87	1	PTHP_STRSL
79	7	1.9	94	1	YR23_HAEIN
80	7	1.9	96	1	PER1_AQUAE
81	7	1.9	99	1	YO10_BHPPI
82	7	1.9	102	1	KCRB_PIG
83	7	1.9	109	1	V42_EPT3
84	7	1.9	115	1	NRG4_MOUSE
85	7	1.9	115	1	NO3M_DUGDU
86	7	1.9	115	1	TKX1_RABIT
87	7	1.9	118	1	YKD7_YEAST
88	7	1.9	119	1	B2MG_HUMAN
89	7	1.9	119	1	B2MG_MACRA
90	7	1.9	119	1	B2MG_PONPY
91	7	1.9	123	1	Y055_MYCGE
92	7	1.9	123	1	YMB2_DEIRA
93	7	1.9	124	1	SPBH_THERN
94	7	1.9	125	1	FRDD_MYCTU
95	7	1.9	130	1	DHSC_PARDE
96	7	1.9	130	1	KVSG_MOUSE
97	7	1.9	130	1	Y060_EPT4
98	7	1.9	130	1	YRFO_ECOLI
99	7	1.9	132	1	YRFO_BACSU
100	7	1.9	134	1	YFID_BACSU

ALIGNMENTS

Q06584	pseudomonas	Q00141	aspergillus
Q01841	gallus gall	P39396	escherichia
Q09465	mus musculus	P18759	saccharomyc
P07798	saccharomyc	Q42484	aradiopsis
Q42484	aradiopsis	Q94377	ricchetti
Q94377	ricchetti	Q94201	candida alb
Q94183	ricchetti	Q94177	ricchetti
Q94182	ricchetti	Q94180	ricchetti
Q94181	ricchetti	Q94179	ricchetti
Q54658	ricchetti	Q62470	mus musculus
P17852	criceidae	P26005	homo sapien
P38097	escherichia	P38438	mus musculus
P38990	saccharomyc	O51578	borrelia bu
P34578	caenorhabdi	O15149	homo sapien
P58107	homo sapien	P15534	notocodarus
P80100	ectothiorho	O16825	drosophila
P21663	drosophila	Q85419	archaeoglob
O52345	mycoplasma	O14211	schistosach
Q08495	xana pipien	Q07502	glycine max
O32223	baecillus su	O76201	phenetria
O76200	phenetria	P45596	streptococc
Q36832	baecillus ha	Q94436	streptococc
P24366	streptococc	P44194	haemophilus
O67065	aquifex aeo	P51712	bacterioph
Q28594	sus scrofa	P20316	bacterioph
Q94944	mus musculus	Q84994	dugong dugo
P15440	oryctolagus	P33858	saccharomyc
P01884	homo sapien	Q84820	macaca fasc
P14213	pongo pygna	P47301	mycoplasma
Q91845	delnoccocus	Q84747	therm
Q10763	mycobacteri	Q59659	paracoccus
P01639	mus musculus	P38222	bacterioph
P76548	escherichia	O31451	baecillus su
P54720	baecillus su		

ALIGNMENTS

RESULT 1

MHC class I lymphocyte antigen - human (fragment)
A:Accession: A24512
A:Molecule type: DNA
A:Residues: 1-342 <DAV>
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C:Accession: 168750
R:Polh, H.; Kuo, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B
A:Reference number: 154457; PMID:89233295; PMID:2714852
A:Accession: 168750
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-290 <RES>
A:Cross-references: GB:M28207; NID:G576478; PIDN:AAA3259.1; PID:G576478
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:144-209/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LVVLAVAL 256
DB 241 LVVLAVAL 248

RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86406
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conny, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nelson, N.F.; Hughes, B.; Hultine, L.
Nature 408, 815-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salazar, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; PMID:121016719; PMID:11130712
A:Accession: A86406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <STO>
A:Cross-references: GB:A605172; NID:G11024872; PIDN:AA626956.1; GSPDB:GN00141
C:Genetics:

A:Map position: 1

Query Match 2.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVAL 257
DB 248 LVVLAVAL 35

RESULT 3

MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1998 #text_change 22-Jun-1999
C:Accession: A24512
R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotide

A:Reference number: A92500; PMID:86033791; PMID:3863816

A:Accession: A24512
A:Molecule type: DNA
A:Residues: 1-342 <DAV>
A:Cross-references: GB:M1886; NID:G184173; PIDN:AAA52655.1; PID:G386777
C:Genetics:
A:Gene: HLA-C
A:Cross-references: GDB:119311; OMIM:142840
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:196-261/Domain: immunoglobulin homology <IMM>
F:86/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LVVLAVAL 256
DB 293 LVVLAVAL 300

RESULT 4

type I restriction enzyme M protein, truncated homolog U098 [imported] - Ureaplasma ure
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002
C:Accession: E82933
R:Glaser, U.I.; Lefkowitz, E.U.; Glaser, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mr
A:Reference number: A82870
A:Accession: E82933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1348 <GLA>
A:Cross-references: GB:A6002110; GB:AF222894; NID:G6899051; PIDN:AAF30504.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: hsdM-1; U098
A:Genetic code: SGC3
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 2.6%; Score 8; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 RKEDIRIV 130
DB 336 RKEDIRIV 343

RESULT 5

class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0546
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
U. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A:Reference number: JH0534; PMID:92078860; PMID:1744581
A:Accession: JH0546
A:Molecule type: DNA
A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60249; NID:G22882; PIDN:CAA42801.1; PID:G22883
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Intons: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>

Mon Apr 12 09:42:27 2004

us-09-831-805a-6.oligo.rpr

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:21:09 ; Search time 21 Seconds
(without alignments)
1419.970 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 310
Sequence: 1 MALRRPPRLICARLPDPFL.....VNIYRDEGDPFKKSFVY 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database :

PIR 78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	290	2	168750
2	8	2.6	336	2	A68406
3	8	2.6	342	1	HLHUC4
4	8	2.6	348	2	E82933
5	8	2.6	366	2	UH0546
6	8	2.6	366	2	UH0547
7	8	2.6	366	2	UH0548
8	8	2.6	366	2	137078
9	8	2.6	492	2	AB1013
10	8	2.6	784	2	A86676
11	7	2.3	77	2	JCS645
12	7	2.3	113	2	AH7748
13	7	2.3	171	2	G70548
14	7	2.3	172	2	T08548
15	7	2.3	173	2	T01282
16	7	2.3	173	2	B90241
17	7	2.3	173	2	T25730
18	7	2.3	177	2	E85833
19	7	2.3	177	2	B90988
20	7	2.3	208	2	T03627
21	7	2.3	208	2	T01588
22	7	2.3	211	2	E86888
23	7	2.3	214	2	T47268
24	7	2.3	217	2	T30446
25	7	2.3	242	2	G84315
26	7	2.3	244	2	A46066
27	7	2.3	255	2	T35883
28	7	2.3	280	2	PH0269
29	7	2.3	294	2	H84023

30	7	2.3	297	2	AB3037	hypothetical prote
31	7	2.3	297	2	A81002	conserved hypothet
32	7	2.3	299	2	A98249	nitrate transport
33	7	2.3	300	2	A82017	probable lipoprote
34	7	2.3	302	2	B70471	heat shock protein
35	7	2.3	306	2	I48139	lymphotoxin-beta -
36	7	2.3	314	2	AG3093	hypothetical prote
37	7	2.3	314	2	C96193	sugar transport sy
38	7	2.3	324	2	T27302	hypothetical prote
39	7	2.3	333	2	I38974	G protein-coupled
40	7	2.3	343	2	H95879	probable sugar ABC
41	7	2.3	346	2	D75303	conserved hypothet
42	7	2.3	362	2	G75614	GDEF family prote
43	7	2.3	375	2	T46378	hypothetical prote
44	7	2.3	376	2	F71815	hypothetical prote
45	7	2.3	380	2	E88421	protein R74.2 (imp
46	7	2.3	382	2	T24963	hypothetical prote
47	7	2.3	391	2	E72539	hypothetical prote
48	7	2.3	392	1	RHUPD	poliovirus recepto
49	7	2.3	392	2	B44194	poliovirus recepto
50	7	2.3	400	2	T24258	hypothetical prote
51	7	2.3	402	2	T04348	endosperm specific
52	7	2.3	402	2	G83367	hypothetical prote
53	7	2.3	403	1	GRECY	tyrosine-specific
54	7	2.3	403	2	G90955	tyrosine-specific
55	7	2.3	403	2	D85804	tyrosine-specific
56	7	2.3	417	1	RHUPA	poliovirus recepto
57	7	2.3	417	2	A44194	poliovirus recepto
58	7	2.3	420	2	T36532	probable membrane
59	7	2.3	421	2	H86217	protein T2767.16 (
60	7	2.3	431	2	D81282	probable efflux pr
61	7	2.3	437	2	AB1849	proton/sodium-glut
62	7	2.3	454	2	JC4616	aprase (EC 3.6.1.1
63	7	2.3	463	2	D84065	glucose-1-phosphat
64	7	2.3	481	2	S68808	lincomycin resist
65	7	2.3	490	2	A96556	probable tRNA-guan
66	7	2.3	491	1	O4R8PC	cytochrome P450 2B
67	7	2.3	491	2	S31277	cytochrome P450 2B
68	7	2.3	491	2	S31278	cytochrome P450 2B
69	7	2.3	491	2	S35666	cytochrome P450 2B
70	7	2.3	503	2	E83490	probable MPS trans
71	7	2.3	504	2	E87628	hypothetical prote
72	7	2.3	523	2	B95922	hypothetical nucle
73	7	2.3	524	2	A31318	glucose transport
74	7	2.3	530	2	C95268	probable ABC trans
75	7	2.3	558	2	B87098	conserved hypothet
76	7	2.3	558	2	G70879	hypothetical prote
77	7	2.3	595	2	H69345	translation initia
78	7	2.3	618	2	A36907	pyocin S1 S1A subu
79	7	2.3	629	2	AD1838	Na+/H+ antiporter
80	7	2.3	643	2	A41120	prostaglandin tran
81	7	2.3	671	2	PH0268	epidermal autoant
82	7	2.3	688	2	H83070	conserved hypothet
83	7	2.3	689	2	D83501	pyocin S2 PA1150 (
84	7	2.3	690	2	C36907	pyocin S2 S2A subu
85	7	2.3	693	1	S39427	NADPH-ferrihemop
86	7	2.3	698	1	A47203	protein-glutamine
87	7	2.3	705	2	T16088	hypothetical prote
88	7	2.3	709	2	C87258	fatty oxidation co
89	7	2.3	716	2	AB1070	probable carbon st
90	7	2.3	721	2	S56580	carbon starvation
91	7	2.3	721	2	A98293	probable carbon st
92	7	2.3	721	2	D86134	probable carbon st
93	7	2.3	741	2	H90507	atp-dependent heli
94	7	2.3	747	2	T40728	hypothetical prote
95	7	2.3	758	1	S45477	SEC18 protein - ye
96	7	2.3	780	2	T29580	hypothetical prote
97	7	2.3	782	2	T44262	transducer protein
98	7	2.3	789	2	E84236	Htr6 transducer (l
99	7	2.3	798	2	T48304	hypothetical prote
100	7	2.3	815	2	H96494	protein F7722.2 (l



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